151 12.9 628 2 T09458 numb-bind numb-bind 12.9 1728 2 T32733 AMPA glut 12.9 1728 2 T32733 AMPA glut 12.9 1728 12.9 1728 2 T32733 AMPA glut 12.9 12.7 2 T14152 PS7 AMPA glut 12.9 12.7 2 T14152 PS7 AMPA glut 12.9 12.7 2 T14152 PS7 AMPA glut 14.5 12.6 505 2 A53214 AS PS	ALIGNMENTS	RESULT 1 T27179 hypothetical protein Y54GilA.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-C R;Wallis, J.	submitted to the EMBL Data Library, December 1998 A;Reference number: 220322 A;Accession: 127179 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA	A.Experimental source: clone Y54G11A C;Genetics: A;Gene: CESP:Y54G11A.10 A;Introns: 55/3; 108/3; 175/3; 228/2; 253/3	Query March 56.6%; Score 662; DB 2; Length 317; Best Local Similarity 68.4%; Pred. No. 2.5e-42; Matches 130; Conservative 30; Mismarches 30; Indels 0;	OY 25 LDRDVARAIELLEKLQESGEVPUHKLQSLKKVLQSEFCTALREVYQYMHETITV	Qy 85 RARATAKATVAAFAASEGHSHPRUVELPKTDEGLGFNVMGGKEQNSPIYISRI] :	Qy 145 RHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMER	Qy 205 TARRRQQQQL 214 Db 297 IRSTQQSPTL 306		A;Status: preliminary; translated from GB/EMBL/DDBJ
GenCore v (c) 1993 - n, using sw 2004, 13:24:	3apop 10.0 , Gapext 0.5 283366 segs, 96191526 residues	hits satisfying chosen parameters: 283366 ength: 0 ength: 0 ength: 2000000000 Minimum Match 0 Maximum Match 00 Listing first 45 summaries	PIR 78:* pir1:* pir2:* pir2:* pir2:* pir3:*	is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.	* Query Match Length DB ID Description	.6 317 2 T27179 .0 1131 2 T15617 .7 852 2 T10811	. 6 8/0 2 0.019/4 Cadanne. 8 720 2 A45436 Synapse. 8 720 2 M46900 postsyr.	.0	.4 2055 2 .9 2054 2 .1 1012 2 .0 431 2	14.7 2466 2 167629 protein-tyrosine-p 14.4 2294 2 167630 protein-tyrosine-p 14.3 126 2 181209 tyrosine phosphata 14.1 12 742372 probable guanylate 14.1 126 2 180209 protein-tyrosine-p 14.1 1256 2 180209 protein-tyrosine-p 14.1 2490 1 A54971 protein-tyrosine-p 13.6 578 2 721345 hypothetical prote 13.6 578 2 721345 hypothetical protein 13.7 423 2 721568 hypothetical protein 13.8 13.7 2 121568 hypothetical protein 13.9 470 2 721568 hypothetical protein	.9 538 2

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C;Species: Drosophils melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-St
C;Accession: A3951
R;Woods, D.F.; Bryant, P.J.
Cell 66, 451-464, 1991
A;Title: The discs-large tumor suppressor gene of Drosophila encodes
A;Reference number: A39651; MUID:91330294; PMID:1651169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: FlyBase:dlg1
A;Gene: FlyBase:FBgn0001624
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; g
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; g
C;Keywords: signal transduction
                 A;Gene: chapsyn-110
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; gr
F;198-276/Domain: GLGF domain homology <GLG2>
F;681-601/Domain: SH3 homology <SH3>
F;681-858/Domain: guanylate kinase homology <GKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A39651
A;Nolecule type: mENA
A;Nolecule type: mENA
A;Residues: 1-960 < WOO>
A;Cross-references: GB:W73529; NID:g157243; PIDN:AAA28468.1; PID:g15
C;Comment: Loss of this protein causes large imaginal disks by allow ction to control cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synapse-associated protein SAP90 - rat
C,Species: Rattus norvegicus (Norway rat)
C,Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-J
                                                                                                                                                                                                                                                                                         43 GEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNGCPEFRARATAKATVAA!
                                                                                                                                                                                                                                                                                                                                                                                                      103 HSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                   418 --EPRKVVLHKGSTGLGFNIVGG-EDGEGIFVSFILAGGPADLSGELQRGDQIL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | ||:| || || :| :: :| ||: || 475 IRGASHEQAAAALKGAGGTVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 GLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 AVPPGTPRAVSTEDITREPRTITIQKGPQGLGFNIVGG-EDGQGIYVSFILAGG
                                                                                                                                                                                                                                        43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 960;
                                                                                                                                                                               Length 870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discs-large tumor suppressor - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 208.5; DB 1;
ilarity 39.3%; Pred. No. 9e-08;
Conservative 21; Mismatches 49;
                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                385 GLLPDSEMTS----HSQHSTATRQPSMTLQRAVSLEG-
                                                                                                                                                                            Query Match
18.6%; Score 217.5; DB 2.
Best Local Similarity 29.3%; Pred. No. 1.7e-08;
Matches 55; Conservative 31; Mismatches 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;45-123/Domain: GLGF domain homology «GLG1»
F;159-241/Domain: GLGF domain homology «GLG2»
F;491-563/Domain: GLGF domain homology «GLG3»
F;607-665/Domain: GLGF domain homology «GLG3»
F;771-948/Domain: guanylate kinase homology «GKI»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 QQQQLLIQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     535 OKRSLYVR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 46; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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iscs-large tumor suppressor; GLGF domain homology; guanylate kinase homo
iscs-large tumor suppressor; GLGF domain homology (GLG)
: GLGF domain homology (GLG)
: SH3 homology (SH3)
: guanylate kinase homology (GKI)
                                             38: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F6
                                                                                                                              210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1
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                                                                                                                                                                                                                                                                                                  VELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR--- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              996 #sequence_revision 06-Jun-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           999 #sequence_revision 16-Jul-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Y.; Takai, Y.
EMBL Data Library, April 1996
loning of new isoforms of PSD-95/SAP90 related genes.
                                                                                                                                                                                                                                              ;
                                                                                                                                                                                       DB 2; Length 1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e kinase ...
18.7%; Score 219; DB 2; Lengum ...
Pred. No. 1.3e-08; ...
-...e 54; Indels
                                                                                                                                                                                                                 ; Pred. No. 1.5e-09;
18; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 <KIM>
es: EMBL:U32376; NID:g1463025; PID:g1036790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         es: EMBL:U53368; NID:g1517939; PID:g1517940
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larity 35.7%; Pred. No. 1.3e-Conservative 24; Mismatches
                                                                                                                                                                                       20.0%; Score 233.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed protein of synapse - human sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | :: | :: | SMSSGSGSLRTNQKRSLYVR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TARREQQQULIQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed protein of synapse 2 - s norvegicus (Norway rat)
                                                                                                                                                                                                                       48.5%;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               er: Zī7166
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                            11 <BEN>
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DNA
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C;Accession: I38757
R;Lue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.
Proc. Natl. Acad. Sci. U.S.A. 31, 9818-9822, 1994
A;Title: Cloning and characterization of hdlg: the human homologue c
A;Reference number: I38756; MUID:95024052; PMID:7937897
A;Accession: I38757
                                                                                                                                                                                                                                                          A, Experimental source: mammary
C, Geneticas:
A, Gene: PSD95
C, Superfamily: discs-large tumor suppressor; GLGF domain homology; g
F, 208-26f Domain: GLGF domain thomology «GLG»
F, 478-556 Domain: GLB homology «GLG»
F, 578-755 Domain: GLB anylate kinase homology «GKL»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homolog of Drosophila discs large protein, isoform 1 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 PRRIVIHRGSTGLGFNIVGG-EDGEGIFISFILAGGPADLSGELRKGDQILSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: EMBL:U13897; NID:g558437; PIDN:AAA50599.1; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR------T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:| :| :| :| :| 523 ASHEQAAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLREQMMNSSISSGSGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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C;Superfamily: discs-large tumor suppressor; GLGF domain homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 16.4%; Score 192; DB 2; Length 904; I Similarity 35.2%; Pred. No. 1.4e-06; 44; Conservative 23; Mismatches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Indels
                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-767 <STA>
A;Cross-references: EMBL:U83192; NID:g3318652; PID:g3318653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:| || || || || 413 ASHEQAAIALKNAGQTVTIIAQYKPEEYSRFEAKIHDLR 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.8%; Score 196.5; DB 2;
41.4%; Pred. No. 5.4e-07;
tive 19; Mismatches 38;
A;Reference number: Z16761
A;Accession: T09599
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: alternative splicing; duplication
C;Keywords: alternative splicing; duplication
F;229-307/Domain: GLGF domain homology <GLG1>
F;324-402/Domain: GLGF domain homology <GLG2>
F;715-895-46/Domain: GHH homology <GKI>
F;715-892/Domain: guanylate kinase homology <GKI>
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A,Cross-references: GDB:393278; OMIM:601014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synapse-associated protein 97 - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
Matches 44; Conserv
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A;Molecule type: mRNA
A;Residues: 1-904 <RES>
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er: JH0800; MUID:93040233; PMID:1419001
                                         R.W.; Cases-Langhoff, C.; Garner, A.M.; Appeltauer, U.
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Sizes-large tumor suppressor; GLGF domain homology; guanylate kinase homo
GLGF domain homology <GLGI>
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                                                  anzel, B.M.; Veb, R.W.; Cases-Langhoff, C.; Garner, A.M.; Appeltauer, U.
38, 4580-4583, 193
a rat presynaptic protein related to the product of the Drosophila tumor
ar: A45436; MUD:93186749; PMID:7680343
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s: brain specific PSD-95 protein; discs-large tumor suppressor protein l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
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Conservative 19; Mismatches 38; Indels
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|BQAAIALKNAGQTVTIIAQYKPEEYSRFEAKIHDLR 408
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.larity 41.4%; Pred. No. 5.1e-07;
Conservative 19; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH3 homology <SH3>
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                                                                                                                                                                                                                                                                                                                      nucleic acid
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Oy 213 QLIIQ 217	Query Match Best Local Similarity 29.0%; Pred. No. 4.2e-06; Bat Local Similarity 29.0%; Pred. No. 4.2e-06; Matches 56; Conservative 31; Mismatches 81; Indels 25; Qy 1 MIKPSVTSAPTADMATLIVVQPLTLDRDVARAIELLEKLQESGEVPVHKL.	OY 117 GLEFWANGGEKONDETILERIE DGGVAERHGGIKKUDLESUNGSVEEH 1981 GLSFNIVGGYGSPHGDLETYVKTVFAKGAAAEDGRLKRGDQITAVNGQSLEGVT: Qy 174 LLKAAKDSVKLVV 186 1	RESULT 13 T46612 multi PDZ domain protein 1 - rat C;Species: Ratus norvegicus [Norway rat) C;Species: Ratus norvegicus [Norway rat) C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-J C;Accession: T46612 R;Ullmer, C.; Schmuck, K.; Figge, A.; Lubbert, H. FEBS Lett. 424, 63-68, 1998 A;Ttle: Cloring and characterization of MUPPl, a novel PDZ domain p A;Reference number: Z23104; MUID:98196865; PMID:9537516 A;Recession: T46612 A;Retuse: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-2054 <ull; a;cross-references:="" a;experimental="" a;genetics:="" a;genetics:<="" brain="" embl:aj001320;="" nid:g2959978;="" pi="" pidn:caa04681.1;="" source:="" th=""><th>Query Match Best Local Similarity 28.5%; Pred. No. 9.9e-06; Matches 55; Conservative 31; Mismatches 82; Indels 25; Qy 1 MLKPSVTSAPTADYATLIVVQPLTLDRDVARAIELLEKLQESGBVPVHKLV </th></ull;>	Query Match Best Local Similarity 28.5%; Pred. No. 9.9e-06; Matches 55; Conservative 31; Mismatches 82; Indels 25; Qy 1 MLKPSVTSAPTADYATLIVVQPLTLDRDVARAIELLEKLQESGBVPVHKLV
s norvegicus (Norway rat.) 396 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000 552 Cistar. U.; Veb, R.W.; Cases-Langhoff, C.; Becker, B.; Gundelfinger, E. 2354-2366, 1955 ar characterization and spatial distribution of SAP97, a novel presynapt 215652; MUID:95198112; PMID:7891172 552 inary; translated from GB/EWBL/DDBJ mRNA 1 <res. 28:="" <glg2.="" domain="" embl.u14950;="" glgf="" guanylate="" homo:="" homology="" homology;="" iscs-large="" kinase="" nid:g642455;="" pid:g642456="" pidn:aaa79976.1;="" suppressor;="" tumor=""> GLGF domain homology <glg2.> GLGF d</glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></glg2.></res.>	HEKAVELIKAAKDSVKLUVRYTPKVLEEMERREKER.RTARRRQQQ 212 - - - - - - - - - - -	isolorm Mar-1996 Chishti, 2, 1994 Alg: the PMID:793	inary mRNA 6 CRES, es: EMBL:U13896; NID:g558435; PIDN:AAA50598.1; PID:g558436 es: GDB:393278; OMIM:601014 3q29-3q29 isca-large tumor suppressor; GLGF domain homology; guanylate kinase homor structive splicing; duplication : GLGF domain homology cGLG1> : GLGF domain homology cGLG2> : GLGF domain homology cGLG3> : GLGF domain homology cGLG2> : GLGF domain homology cGLG3> : GLGF domain homology c	VVELPKTDEGLGFNVWGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSUG 165 :

SEFCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDE 116	Matches 45; Conservative 26; Mismatches 46; Indels 14;
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GENVWGGKEQNSPIXISRIIPGGVAERHGGLKRGDQLLSVNGVSUFGEHHEKAUE 173	36
GFSIVĠĠYGSPHGDLPIYVKTVFAKGAAAEDĠRLKRĠDQIIAVNĠQSLEGVTHEEAVA 2039	Qy 165 GEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLRTA
KARALISVALIV 186 KARALISVALIV 186 KARALISVALIV 2062	
	156
tein KOLA6.1 - Caenorhabditis elegans rhabditis elegans 999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000 160	Search completed: March 18, 2004, 13:28:52 Job time : 21 secs
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inary; translated from GB/EMBL/DDBJ DNA. 12 <ni. 12="" <ni.="" cesp:k01a6.1="" clone="" ebbl:z68750;="" gspdb:gn00022;="" k01a6<="" ource:="" pidn:caa92965.1;="" td=""><td></td></ni.>	
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; 151/2; 183/2; 270/2; 316/3; 410/3; 628/3; 922/3; 971/3 W repeat homology : WW repeat homology <wwr></wwr>	
15.1%; Score 177; DB 2; Length 1012; ilarity 32.4%; Pred. No. 2.2e-05; Conservative 30; Mismatches 50; Indels 20; Gaps 6;	
LKKVLQSEFCTAIRSUVQYMHETITVNGCPEFRARATAKATVAAFAASEGHS 104 ::	
RVVELPKTDEGLGFNVMGGKEQNSPIXISRIIPGGVAERHGGLKRGDQLLSVNGV 161	
EGEHHEKAVELLKAAKDSVKLVVR 187	
tein F27D9.8 - Caenorhabditis elegans rhabditis elegans 999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 191	
EMBL Data Library, February 1996 he sequence of C. elegans cosmid F27D9.	
1191 inary; translated from GB/EMBL/DDBJ DNA	
.1 <ben>: - SENS CESP:F27D9 CESP:F27D9</ben>	
'D9.8 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3	
15.0%; Score 176; DB 2; Length 431; nlarity 34.4%; Pred. No. 9.3e-06;	

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Copyright (c) 1993 - 2004 Compugen Ltd.
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SwissProt_42:*

SUMMARIES ū Query Match Length DB

063622 rattus norv 205700 homo sapien P31007 drosophila Q22796 homo sapien P70175 mus musculu 06296 rattus norv 062108 mus musculu 062696 rattus norv 01295 homo sapien 01295 homo sapien 02918 mus musculu 092340 rattus norv 0213425 homo sapien 099188 mus musculu 092188 mus musculu 099188 mus musculu 099188 mus musculu 099188 mus musculu 099189 homo sapien 054065 homo sapien 054065 homo sapien 062666 pant troqlod P57105 homo sapien 062666 mus musculu 099188 mus musculu 099189 homo sapien 062666 mus musculu 066866 mus musculu 066866 mus musculu homo sapien mus musculu homo sapien Q86ul8 homo sapien Q925e0 mus musculu Q8tbbl homo sapien Q28626 oryctolagus mus musculu mus musculu rattus norv Description 09wvq1 t Q13884 O70263 DLG1_DROME
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ALIGNMENTS

PR001478; PDZ

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                                           MEDLINE-96310881; PubMed-8755482; Kim E., Cho K.-O., Rothschild A., Sheng M.; Cho K.-O., Rothschild A., Sheng M.; Heteromultimerization and NMDA receptor-clustering activity of Chapsyn-110, a member of the PSD-95 family of proteins."; Neuron 17:103-113(1996).
                                                                                                                                                                     -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPS SUBUNITS AS WELL AS POTASSIUM CHANNELS.
-!- SIMILARITY: Belongs to the MAGUK family.
-!- SIMILARITY: Contains 3 PDZ/DHR domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GEVPVHKLOSLKKVLOSEFCTAIREVYQYMHETITVNGCPEFRARATAKATVAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                418 --EPRKVVLHKGSTGLGFNIVGG-EDGEGIFVSFILAGGPADLSGELQRGDQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 HSHPRVVELPKIDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.6%; Score 217.5; DB 1; Length 870; 29.3%; Pred. No. 2.9e-08; Live 31; Mismatches 59; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 GLLPDSEMTS----HSQHSTATRQPSMTLQRAVSLEG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06 SH3.
370 GUANYLATE KINASE.
97500 MW, 89C83BA0619F6F59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004385; F:guanylate kinase activity; TAS.
InterPro; IRR008144; Guanylate kin.
InterPro; IRR008145; Guanylate kin.
InterPro; IRR001478; PDZ.
InterPro; IRR001478; PDZ.
InterPro; IRR001478; SH3.
Pfam, PP00625; Guanylate kin; 1.
Pfam, PP00655; PDZ; 3.
Pfam, PP00618; SH3; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 VEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00072; GuKC; 1.
SWART; SM00072; GuKC; 1.
SWART; SM00326; SH3; 1.
PROSITE; PS00856; GUANYLATE KINASE 1; 1.
PROSITE; PS00052; GUANYLATE KINASE 2; 1.
PROSITE; PS50006; PDZ; 3.
PROSITE; PS50006; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32376; AAB04949.1; -.
PIR; G01974; G01974.
HSSP; Q12959; 1PDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:2901; DLG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279
501
606
870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 OQQQLLIQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 QKRSLYVR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      870 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3 domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
536
680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 603583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
NAMES OF STREET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROPSVILORAISLEGEPRKVVLHKGSTGLGFNIVGG-EDGEGIFVSFILAGGPADLSG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR--- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 42, Last amoutation update)
(Cel. 42, Last amoutation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Witheria; Primates; Catarrhini; Hominidae; Homo.
19606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.7%; Score 219; DB 1; Length 852; 35.7%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              870 AA.
                                                                      95; PD2; 3. — 18; SH3; 1. 00066; SH3; 1. 00066; SH3; 1. 072; Gukc; 1. 228; PDZ; 3. 326; SH3; 1. 00856; GUANYLATE_KINASE_1; 1. 50052; GUANYLATE_KINASE_2; 1. 80002; SH3; 1. Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSMSSGSGSLRTNQKRSLYVR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TARREQUOLLIQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                        PR001452; SH3.
25; Guanylate_kin; 1.
```

Conservative

ilarity

852 AA;

STANDARD;

is (Human).

43;

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Makino K., Kuwahara H., Maguko N., Nishiyama Y., Morisaki T., Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.; Saloning and characterization of NE-dlg: a novel human homolog Drosophila discs large (dlg) tumor suppressor protein interacte the APC protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 GLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 ELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLLAQYRPEEYNRFEARIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Prediction of the coding sequences of unidentified human genes
The complete sequences of 100 new cDNA clones from brain which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 17.8%; Score 208.5; DB 1; Length 960; Local Similarity 39.3%; Pred. No. 1.4e-07; les 46; Conservative 21; Mismatches 49; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Presynaptic protein SAP102 (Synapse-associated protein 102) (Neuroendocrine-DLG) (NE-DLG) (Discs, large homolog 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       102468 MW; BF87A4262F1B6AD5 CRC64;
                                                                                                                                                                                                                                                                                                                 domain; Alternative splicing; Repeat. 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIGS HULTIS

092756, ODULIS;

01-NOV-1997 (Rel. 35, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT NR2B (BY SIMILARITY).
SIMILARITY: Belongs to the MAGUK family.
SIMILARITY: Contains 3 DDZ/DHR domains.
                                                                                                                                                                                                                        PROSITE; PS00856; GUANYLATE KINASE 1; 1. PROSITE; PS50052; GUANYLATE KINASE 2; 1. PROSITE; PS50006; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20039619; PubMed=10574462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97332623; PubMed=9188857;
                                            InterPro; IPR001452; SH3.
Pfam; PF00625; Guanylate_kin; 1.
Guanylt/Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete sequences of 100 n
large proteins in vitro.";
Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 330-817 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 14:2425-2433 (1997).
                                                                                      Pfam; PF00595; PDZ; 3.
Pfam; PF00018; SH3; 1.
ProDom; PD000066; SH3; 1.
                                                                                                                                                           SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       960 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLG3 OR KIAA1232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              154
486
600
                                                                                                                                                                                                                                                                                                                      Fransducer; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLG3 HUMAN
                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
DLG3 HUMAN
                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Matches
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROT entry is copyright. It is produced through a collaboration e Swiss Institute of Bicinformatics and the EMBL outstation n Bioinformatics Institute. There are no restrictions on its n-profit institutions as long as its content is in no way it this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n-profit institutions as long as its content is in no way d this statement is not removed. Usage by and for commercial quires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epithel. .; NAS. polarit. .; IGI. polarit. .; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N: Plays a critical role at septate junctions in cellular sontrol during larval development. The presence of a se kinase domain suggests involvement in cellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIFICITY: In embryos, expression is seen in epithelial and some nervous tissue. In larvae, expression is seen as a ound salivary glands and imaginal disks, also in riculus and parts of the brain. Expressed in adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as signal transduction to control cellular proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE SMIC PACE OF THE MEMBRANE IN THE CELLULAR BLASTODERM AND ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM PEPTHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MENTAL STAGE: Expressed both maternally and zygotically
                                                                                                                                                                                                                                                                                                                                                                                                                               large tumor suppressor gene of Drosophila encodes a inase homolog localized at septate junctions.";
                                                                                                                                                                                                     nelanogaster (Fruit fly).
Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
ndopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     out development. TITY: Belongs to the MACUK family. ITY: Belongs to the MACUK family. ITY: Contains 3 PDZ/DHR domains. ITY: Contains 1 SH3 domain. ITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191; P:dorsal closure; NAS.

197; P:establishment and/or maintenance of 334; P:establishment and/or maintenance of 336; P:establishment and/or maintenance of 339; P:neurogenesis; IMP.

273; P:regulation of synapse; IMP.

PR008144; Guanylate kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; 1BFE.
gn0001644; dlg1.
179; C:apical cortex; IDA.
327; C:apicolateral plasma membrane; IDA.
918; C:esptare junction; NAS.
175; P:basal protein localization; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lternative splicing; Named isoforms=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nt=A number of isoforms are produced;
                                                                                                                                        Last annotation update)
                                                 960 AA.
                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               =P31007-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           ; Drosophilidae; Drosophila.
                                                                                                                                                               1 tumor suppressor protein.
                                                                                                                                                                                                                                                                                                                                                                                          30294; PubMed=1651169;
                                                                                                                                                                                                                                                                                                                                             OM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as signal transduct
                                                                                             [Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; AAA28468.1; -.
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ctive tissues.

A39651

TIVE PRODUCTS

-464(1991).

DIGI

817 AA.

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062936; P70547;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Presynaptic protein SAP102 (Synapse-associated protein 102) (PS
95/SAP90 related protein 1) (Discs, large homolog 3).
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictiuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.cor or send an email to license@isb-sib.ch).
                                                                                                                                              œ
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57EL/6; TISSUE-Brain;
Kohmura N., Makino S., Yagi T.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA F
SUBMIT NR.B.
SUBMIT NR.B.
- SUBCITE SELONGS to the MAGUK family.
- PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 PRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.4%; Score 203.5; DB 1; Length 849; 43.4%; Pred. No. 2.8e-07; tive 18; Mismatches 37; Indels 1;
                                                                                                                                                                                               -!- SIMILARITY: Belongs to the MAGUK family.
-!- SIMILARITY: Contains 3 POZ/DHR domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93482 MW; EF3EF2D7513538EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 ATHEQAAALKRAGQSVTIVAQYRPEEYSRFESKIHDLR 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               849 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPROJ INTERCOLATOR OF THE PRODUCT OF THE PROSTER PRODUCT OF THE PROSTER PRODUCT OF THE PROSTER PRODUCT OF THE PROSTER PROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGZ:1888896; D1gh3.

MGD; MGZ:1888896; D1gh3.

GO; GO:0005737; C:cyroplasm; IDA.

GO; GO:005515; F:protein binding; IPI.

InterPro; IPR008144; Guanylate kin.

InterPro; IPR008145; Guanylate kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDZ 1.
PDZ 2.
PDZ 3.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D87117; BAA13249.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519 56
659 84
849 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
DLG3_RAT
ID DLG3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
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                                                                            PROT entry is copyright. It is produced through a collaboration e Swiss Institute of Bioinformatics and the EMBL outstation - n Bioinformatics Institute. There are no restrictions on its ruprofit institutions as long as its content is in no way d this statement is not removed. Usage by and for commercial quires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFPGLSDDYYGAKNL -> SIKTKRKKSFRLSRKFPFYKSK
ENMAQESSIQEQGVTSNTSDSESSS (IN REF. 2).
3D7512EC4713FC4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRHMLAEEDFT -> AARRERGAMERARKFSGSGLAMGLGS
ASASAWRRASQRWAWPLRSLRPGGDA (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUANYLATE KINASE.
FTALADNHISHNSSLGYLGAVESKVSYPAPPQVPPTRYSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Synapse-associated protein 102) (Discs,
                                                                                                                                                                                                                                                                                                                                                                                                                                      385; F:guanylate kinase activity; NAS. 285; P:negative regulation of cell proliferation; NAS. PRO08144; Guanylate kin. PR008144; Guanylt/Ca. PR0081478; Guanylt/Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, utheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.4%; Score 203.5; DB 1; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches 37; Indels
  ITY: Contains 1 SH3 domain.
ITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.7e-07
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(Rel. 35, Last sequence update)
protein SAPIO2 (Synapse-associated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   849 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00856; GUANYLATE KINASE 1; 1.
50052; GUANYLATE KINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDZ 1.
PDZ 2.
PDZ 3.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Guanylate_kin; 1.
95; PDZ; 3.
                                                                                                                                                                                                                                                                                                  9; AAB61453.1; -.
058; BAA86546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              817 AA; 90344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.48;
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50106; PDZ; 3. 50002; SH3; 1.

Repeat.

465 568 803

909

592

Conservative

ilarity

STANDARD;

og 3). H3. s (Mouse).

100001

18; SH3; 1. 00066; SH3; 1.

072; GuKc; 1. 228; PDZ; 3.

PR001452; SH3

:2902; DLG3.

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DLG4 MOUSE
                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROT entry is copyright. It is produced through a collaboration to Swiss Institute of Bioinformatics and the EMBL outstation - in Bioinformatics Institute. There are no restrictions on its in-profit institutions as long as its content is in no way id this statement is not removed. Usage by and for commercial equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                                                                                                                                                                                                      ta Y., Takai Y.;
SEP-1996) to the EMBL/GenBank/DDBJ databases.
N: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          utheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                            (., Kistner U., Kindler S., Chung W.J., Kuhlendahl S.,
., Lau L.-F., Veh R.W., Huganir R.L., Gundelfinger E.D.,
                                                                                                                                                                                                                        novel postsynaptic protein that interacts with NMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IITY: Belongs to the MAGÜK family.
IITY: Contains 3 PDZ/PHR domains.
IITY: Contains 1 SH3 domain.
IITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform Short). /FTId=VSP 003151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849 AA; 93539 MW; 34DA9C46C7BB96DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            TIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANYLATE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =Q62936-2; Sequence=VSP 003151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    =Q62936-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100856; GUANYLATE KINASE 1; 1. S50052; GUANYLATE KINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                       OM N.A. (ISOFORM SHORT).
ta Y., Takai Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR008144; Guanylate_kin.
                                                                       OM N.A. (ISOFORM LONG).
                                                                                                                     74358; PubMed=8780649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Guanylate_kin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR008145; Guanylt/Ca.
                                                                                                                                                                                                                                                     mplexes in vivo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; AAA93031.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350106; PDZ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PR001478; PDZ.
PR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          072; GuKc; 1.
                                                                                                                                                                                                                                                                         55-265 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity
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STRAIN—BBA/2; ITSUE=Brain; Kohmura N. Yaqi T.; Kohmura N. Yaqi T.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Interacts with the cytoplasmic tail of NWDA recensibilities. May be involved in synaptogenesis.

-!- SUBNUTI: Interacts with DLGARP1/GRAP and with RCNDZ (By similarity). Is part of a complex with DLGAPL/GRAP or SHANKI or SHANKI (By similarity). Interacts through its third PDZ with NLGAN, and probably with NLGANZ and NLGAN: Intracts this first PDZ domain with GRIX2, KCNA4 and CRIPT: Intracts this first PDZ domain with GRIX2, KCNA4 and CRIPT: Intracts this chicult its second PDZ domain with NOSI and CAPON (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict. Uses by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                OL-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2014 (Rel. 43, Last annotation update)
(Synappse-associated protein 95 (PSD-95) (Presynaptic protein Si Dig4 OR DigH4 OR PSD95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLUIAR LOCATION: Cytoplasmic. Concentrated at synaptic junctions primarily on the presynaptic side. Also found in postsynaptic density of neuronal cells (By similarity).
-!- SIMILARITY: Belongs to the MAGUK family.
-!- SIMILARITY: Contains 3 PDZ/DHR domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostor
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7EFFC99E1FFF90BA CRC64;
                     461 ATHEQAAAALKRAGQSVIIVAQYRPEEYSRFESKIHDLR 499
166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUANYLATE KINASE
                                                                                                                                  724 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00056; GUANYLATE KINASE 1; 1. PROSITE; PS50052; GUANYLATE KINASE 2; 1. PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ 1.
PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008144; Guanylate kin.
InterPro; IPR008145; Guanylt/Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fam; PF00625; Guanylate_kin; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D50621; BAA09297.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P31016; 1BE9.
MGD; MGI:1277959; Dlgh4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001478; PDZ
InterPro; IPR001452; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00595; PDZ; 3.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534 7
724 AA;
                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH3 domain; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                DLG4 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
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similarity). Interacts through its second PDZ domain with N CAPON. Interacts with KCND2.
SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic junctions primarily on the presynaptic side. Also found in postsynaptic density of neuronal cells.
IISSUE SPECIFICITY: PRESYNAPTIC DENSITY FRACTION OF BRAIN. SIMILARITY: Belongs to the MAGNK family.
SIMILARITY: Contains 3 PDZ/DHR domains.
SIMILARITY: Contains 1 SH3 domain.
SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute: There are no restrictiuse by non-profit institutions as long as its content is used in this statement is not removed. Usage by and for endities requires a license agreement (See http://www.isb-sib.corer end an email to license@isb-sib.ch).
[7]

REDINGTURE BY NWR OF 155-246, AND INTERACTION WITH NOSI AND CAPO MEDLINE-20090929; PubMed=10623522;
Tochio H., Hung F., Li M., Bredt D.S., Zhang M.;
"Solution structure and backbone dynamics of the second PDZ dom
                                                                                                                                                                                       MEDLINE=21638676; PubMed=11779504; McGee A.W., Dakoji S.R., Olsen O., Bredt D.S., Lim W.A., Prehod McGee A.W., Dakoji S.R., Olsen O., Bredt D.S., Lim W.A., Prehod Structure of the SH3-guanylate kinase module from PSD-95 sugge mechanism for regulated assembly of MAGUK scaffolding proteins. Mol. Cell 8:1291-1301(2001).
                                                                                                                                                                                                                                                                                                                                       MEDLINE=21638678; PubMed=11779506;
Tavares G.A., Panepucci E.H., Brunger A.T.;
"Structural characterization of the intramolecular interaction
                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 430-724.
                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 430-724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SM00228; PDZ; 3.
SWART; SM00326; BH3.
PROSITE; PS00856; GUANYLATE KINASE 1; 1.
PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008144; Guanylate_kin.
InterPro; IPR008145; Guanylt/Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3 domain; Repeat; 3D-structure.

DOMAIN 65 151 PDZ 1.

DOMAIN 160 246 PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 3.
                                                                                                                            J. Mol. Biol. 295:225-237(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M96853; AAA1971.1; -.
EMBL; X66474; CAA47103.1; -.
EMBL; U77090; AAB38270.1; -.
PIR, JH0800; JH0800.
PDB; 1BE9; 21-OCT-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000066; SH3; 1.
SMART; SM00072; GuKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50106; PDZ; 3. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001452; SH3
                                                                                                           postsynaptic density-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDB; 1BFE; 21-OCT-98.
PDB; 1JXM; 16-JAN-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; 1KJW; 01-MAY-02.
PDB; 1QLC; 06-FEB-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro;
      VVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                RIVIHRGSTGLGFNIVGG-EDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M., Winter C., Smalla K.-H., Kreutz M.R., Bockmann J., r. C., Garner C., Gundelflinger E.D.; ch synapse-associated proteins ProSAP1 and ProSAP2 interact ic proteins of the SAPAP/GKAP family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70509; PubMed=8674113; Lee A., Lewis J., Kim E., Sheng M., Mackinnon R.; Lee A., Lewis J., Kim E., Sheng M., Mackinnon R.; ructures of a complexed and peptide-free membrane protein-anin: molecular basis of peptide recognition by PDZ."; 7-1076(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   egicus (Rat).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37905; PubMed=11923279; well E.W., Jugloff D.G.M., Jones O.T., Schlichter L.C.; ice targeting and clustering interactions between taly expressed PSD-95 and the Shal voltage-gated potassium 4.2.";
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 26, Last sequence update)
(Rel. 43, Last annotation update)
density protein 95 (RSD-95) (Presynaptic protein SAP90)
sociated protein 90) (Discs, large homolog 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wenzel B.M., Veh R.W., Cases-Langhoff C., Garner A.M., U., Voss B., Gundelfinger B.D., Garner C.C., at presynaptic protein related to the product of the tumor suppressor gene dlg-A."; em. 268:4580-4583 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ain postsynaptic density fraction contains a homolog of
                                                                   .
;
                          Length 724;
                                                                   38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Werny I., Schwartz S.M.;
NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discs-large tumor suppressor protein.";
                                                                                                                                                                                                                   HEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ar Kyoto, TISSUE=Vascular smooth muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLOGRAPHY (1.82 ANGSTROMS) OF 302-402.
                     ; Score 196.5; DB 1;
; Pred. No. 7.5e-07;
19; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ophys. Res. Commun. 264:247-252(1999)
                                                                                                                                                                                                                                                                                                                                            724 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH DLGAP1 AND SHANK PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .em. 277:20423-20430(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gue-Dawley; TISSUE=Brain;
86749; PubMed=7680343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gue-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40233; PubMed=1419001;
Hunt C.A., Kennedy M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58653; PubMed=10527873;
                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 26, Created)
(Rel. 26, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566-625 FROM N.A.
                          16.8%;
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH KCND2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM N.A.
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VVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                   GUANYLATE KINASE.,

** - L. (IN REF. 2).

$ - X (IN REF. 2).

$ GVGNQH -> ALGTSI (IN REF. 2).

$ - X (IN REF. 2).

$ - X (IN REF. 2).

$ - X (IN REF. 2).

LGPTKORANDDLISEF -> SLDPPKTVPTMIPSPSS (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .., Bredt D.S., Parkinson J.F., Manzana W.P., McClary J.A.; AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ary gland;
32822; PubMed=9286702;
3.6., Hoover K.B., You Z., Bryant P.J.;
synaptic density-95 (PSD95): location of the gene (DLG4)
e function in nonneural as well as in neural tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ganization of human DLG4, the gene encoding postsynaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WITH NLGNI; NLGNZ AND NLGN3.
126629; PubMed=9278515;
tta Y., Takeuchi M., Ichtchenko K., Toyoda A., Hirao K.,
cosahl T.W., Suedhof T.C.;
ineuroligins to PSD-95.";
11511-1515(1997).
                                                                                                                                                                                                                                                                                                                               (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 43, Last annotation update)
(Rensity 195).
ic density 95).
is (Human)
Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47407; PubMed=10582582;
J.G., Udar N., Sandgren O., Andreasson S., Bryant P.J.,
'orsman-Semb K.;
                                                                                                                                                                  1;
                                                                                                                                        16.8%; Score 196.5; DB 1; Length 724; 41.4%; Pred. No. 7.5e-07; tive 19; Mismatches 38; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ary gland;
.G., Hoover K.H., You Z., Bryant P.J.;
JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                          GKH -> RDQ (IN REF. 3).
7922D4E8E0F9AD85 CRC64;
                                                                                                                                                                                                                                             |||:| || || :| :: :| || HEQAAIALKNAGQTVTIIAQYKPEEYSRFEAKIHDLR 408
                                                                                                                                                                                                                                 HEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                             767 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73:2250-2265(1999).
                                                                                                                     80465 MW;
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                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
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393
724
724
61
78
182
200
254
555
                                                                                                                                                                                                                                                                                                                       Q9UKK8;
                                                                                                                      724 AA;
                                                                                                                                                       ilarity
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1. J. Biol. Chem. 277:6967-6973 (2002).

1. J. Biol. Chem. 277:6967-6973 (2002).

1. FUNCTION: Interacts with the cytoplasmic tail of NMDA recep subunits. May be involved in synaptogenesis.

2. SUBUNIT: Interacts with DLGAPL/GRAP and with KCNDZ (By similarity). Is part of a complex with DLGAPL/GRAP. SHANKI.

3. STANKA: Interacts through its second PDZ domain with NK CAPON (By similarity). Bluds to KIFA13B. Interacts through it third PDZ domain with NLGNI, and probably with NLGNZ and NI Intracts through if first PDZ domain with GRIKZ, KCNA4 and Intracts through it of the Korpiasmic. Concentrated at synaptic junctions primarily on the presynaptic side. Also found in presynaptic density of neuronal cells (By similarity).

2. SIMILARITY: Contains 3 PDZ/DHR domains.

3. SIMILARITY: Contains 1 SH3 domains.

3. SIMILARITY: Contains 1 SH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a conserveen the Swiss Institute of Bioinformatics and the EMBL the Buropean Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.corsend an email to license@isb-sib.ch).
[6]
STRUCTURE BY NWR OF 105-197, AND INTERACTION WITH GRIK2; KCNA4
                                                                                              MEDLINE=21850665, PubMed=11744724, Piserchio A., Pellogrini M., Mehta S., Blackman S.M., Garcia : Piserchall J., Mierke D.F., "The PDZI domain of SAP90. Characterization of structure and "The PDZI domain of SAP90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; 60:0004384; F:membrane-associated guanylate kinase; TAS. GO; 60:0008022; F:protein C-terminus binding; TAS. GO; 60:0007612; P:learning; TAS. GO; 60:0007612; P:learning; TAS. GO; 60:0007612; P:learning; TAS. GO; 60:000761; P:protein complex assembly; TAS. GO; 60:000766; P:signal transduction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E -> V (IN REF. 3).
VIV -> EFR (IN REF. 4).
GDQ -> AGI (IN REF. 4).
; BE1019159E65B2D8 CRC64;
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GUANYLATE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00856; GUANYLATE KINASE_1; 1.
PROSITE; PS50002; GUANTLATE KINASE_2; 1.
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
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PDZ 2.
PDZ 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008144; Guanylate kin.
InterPro; IPR008145; Guanylt/Ca.
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InterPro; IPR001452; SH3.
Pfam; PF00655; Gunnylate kin; 1.
Pfam; PF006595; PDZ; 3.
Pfam; PF00018; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U83192; AAC52113.1; -.
EMBL; AF156495; AAD56173.1; -.
EMBL; U68138; AAB07736.1; -.
PIR; T09599; T09599.
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SMART; SM00072; GuKc; 1.
SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1KEF; 06-MAR-02.
Genew; HGNC:2903; DLG4.
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81
399
4767 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 602887
                                                                                                                                                                                                                           binding.";
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CONFLICT
SEQUENCE
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Presynaptic protein SAP97 (Synapse-associated protein 97) (Disc. large homolog 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIPDDMGSKGLK -> QSFNDKRKKNLFSRKFPF
EQETSDADQ (in isoform 2).
/FTId=VSP 003150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR------TA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 ASHEQAAALKNAGQAVTIVAQYRPEEYSRFEAKIHDLREQMMNSSISSGSGSL
  GO:0005886; C:plasma membrane; TAS.
GO:0008092; F:cytoskeletal protein binding; TAS.
GO:0004385; F:guanylate kinase activity; TAS.
GO:0004384; F:membrane_associated guanylate kinase; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.4%; Score 192; DB 1; Length 904; 35.2%; Pred. No. 2e-06; ive 23; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100354 MW; B78798D6BB0920D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3 domain; Repeat; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUANYLATE KINASE.
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PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
GO; GO:0005886; C:plasma membrane; TAK
GO; GO:0008092; F:cytoskeletal protein
GO; GO:0004885; F:cytanylate kinase act
GO; GO:0004384; F:membrane-associated
InterPro; IPR008144; Guanylate kin.
InterPro; IPR008145; Guanylt/Cā.
InterPro; IPR004172; L27.
InterPro; IPR004172; L27.
InterPro; IPR001478; P27.
Fam; PF00525; Guanylate_kin; 1.
Pfam; PF00555; PDZ; 3.
Pfam; PF000185; SH3; 1.
Probon; PD0001665; SH3; 1.
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PDZ 2.
PDZ 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS50052; GUANYLAY
PROSITE; PS50106; PDZ; 3.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                SMART; SM00072; GUKc; 1.
SMART; SM00569; L27; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00228; PDZ; 3.
SMART; SM00326; SH3; 1.
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904 AA;
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 QLLIQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 SLYVR 587
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525
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DLG1_RAT
ID _DLG1_RAT
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SEQUENCE
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          OOR BENEFITTE TETTE TETT
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                                                                                                                         VVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165
                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s (Human).
Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
utheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Discs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arfatia S.M., Branton D., Chishti A.H.;
d characterization of hdig: the human homologue of th
discs large tumor suppressor binds to protein 4.1.";
Acad. Sci. U.S.A. 91:9818-9822(1994).
                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Petosa C., Sutcliffe M.J., Raza S., Byron O., Poy M., Chishti A.H., Liddington R.C.; ructure of a PDZ domain.";
                             Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
protein SAP97 (Synapse-associated protein 97)
og 1) (hDlg).
                     16.8%; Score 196.5; DB 1; Length 7 41.4%; Pred. No. 8e-07; ive 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITY: Contains 3 PDZ/DHR domains.
ITY: Contains 1 SH3 domain.
ITY: Contains 1 guanylate kinase-like domain.
                                                                                                                                                                                                                                HEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                             549-652(1996).
N: INTERACTS WITH THE CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLOGRAPHY (2.8 ANGSTROMS) OF 460-555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 737; C:cytoplasm; TAS.
911; C:intercellular junction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        =Q12959-2; Sequence=VSP_003150;
ITY: Belongs to the MAGUK family.
ITY: Contains 3 PDZ/DHR domains.
ITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                            904 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. ASSOCIATES WITH PROTEIN 4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -Q12959-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24052; PubMed=7937897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38231; PubMed=8757139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Binds to KIF13B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; AAA50599.1; -. 6; AAA50598.1; -.
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIVE PRODUCTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.4(
Protein tyrosine phosphatase 1B) (PTP-B1) (hPTPB1) (PTP-BAS)
(Protein-tyrosine phosphatase PTPL1) (Fas-associated protein-t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95014139; PubMed=7929060; Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.; Cloning and characterization of PTPLI, a protein tyrosine phoswith similarities to cytoskeletal-associated proteins."; J. Biol. Chem. 269:24082-24089(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94116677; PubMed=8287977; Marada S.; Maekawa K., Imagawa N., Nagamatsu M., Harada S.; "Molecular cloning of a novel protein-tyrosine phosphatase cont a membrane-binding domain and GLGF repeats.";
        463 PRKVVLHRGSTGLGFNIVGG-EDGEGIFISFILAGGPADLSGELRKGDRIISV
                                               166 EHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR------T)
                                                                        PIND HUMAN STANDARD; PRT; 2485 AA.
Q12923; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q8IWH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostor
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banville D., Ahmad S., Stocco R., Shen S.-H.;
A novel protein-tyrosine phosphatase with homology to both the
Cytoskeletal proteins of the band 4.1 family and junction-assoc
guanylare knasess.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato T., Irie S., Kitada S., Reed J.C.;
"FAP-1: a protein tyrogine phosphatase that associates with Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang H.Y.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Irie S., Hachiya T., Sato T.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 269:22320-22327(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Bye;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94350988; PubMed=8071359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIPNIS OR PIPIE OR PIPLI OR PNPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95232528; PubMed=7536343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1323-1821 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1216-2490 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1323-1922 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS Lett, 337:200-206(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 268:411-415(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                            213 QLLIQ 217
                                                                                                                                                                      582 SLYVR 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphatase 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang H.Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROT entry is copyright. It is produced through a collaboration e Swiss Institute of Bioinformatics and the EMBL outstation in Bioinformatics Institute. There are no restrictions on its urporfit institutions as long as its content is in no way id this statement is not removed. Usage by and for commercial equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             ULAR LOCATION: IN CULTURED T84 CELLS, IT IS RESTRICTED TO PELASMIC SURFACE OF THE PLASMA MEMBRARES BETWEEN ADJACENT BUT NOT AT THE EDGES OF CELLS LACKING CELL-CELL CONTACT SPECIFICITY: PRESTMAPTIC NENUE TERMINI OF EXCITAORY S. IN OTHER BRAIN REGIONS, SAP97 IS FOUND IN AND ALONG OF UNMELLINATED AXONS. SAP97 IS NOT RESTRICTED TO THE CNS, ALSO PRESENT AT THE BASAL LATERAL MEMBRANE BETWEEN A COF EPITHELIAL CELLS.

ITY: Belongs to the MAGUK family.

ITY: Contains 3 PDZ/DHR domains.

ITY: Contains 1 SH3 domain.

ITY: Contains 1 SH3 domain.
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regicus (Rat).
Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Autheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                           tumor suppressor protein.";
...15.2254-236(1995).
N: INTERACTS WITH THE CYTOPLASMIC TAIL OF NWDA RECEPTOR.
S. MAY BE INVOLVED IN SYNAPTOGENESIS. MAY PLAY A ROLE IN
                                                                                                                                                            4., Kistner U., Veh R.W., Cases-Langhoff C., Becker B., Tr E.D., Garner C.C., Characterization and spatial distribution of SAP97, a maptic protein homologous to SAP90 and the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100570 MW; 18CEBD31DD0CAF8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUANYLATE KINASE.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00856; GUANYLATE KINASE 1; 1.
50052; GUANYLATE KINASE 2; 1.
50106; PDZ; 3.
50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDZ 1.
PDZ 2.
PDZ 3.
SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; IPDR.
PR008144; Guanylate kin.
PR008145; Guanylt/Ca.
                                                                                                                                         198112; PubMed=7891172;
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PR001478; PDZ.
PR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             072; GuKc; 1.
569; L27; 1.
228; PDZ; 3.
326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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18; SH3; 1.
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650
911
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Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structum Domain splicing; Coiled coil; Polymorphism.

PODA-LEU.

POLY-LEU. SIMILARITY: Contains 1 FERM domain.
SIMILARITY: Contains 5 PDZ/DHR domains.
SIMILARITY: Belongs to the protein-tyrosine phosphatase fan Non-receptor class subfamily. GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS. GO; GO:0006470; P:protein amino acid dephosphorylation; TAS. 14.4%; Score 169; DB 1; Length 2485; 28.4%; Pred. No. 0.0003; tive 26; Mismatches 43; Indels 32 Isold=012923-4; Sequence=VSP 007921; Note=May be due to a competing donnor splice site; TISSUB SPECIFICITY: Present in most tissues with the ethe liver and skeletal muscle. Most abundant in lung, PROTEIN-TYROSINE PHOSPHATASE. COILED COIL (POTENTIAL). COILED COIL (POTENTIAL). IsoId=Q12923-2; Sequence=VSP_000496; IsoId=012923-3; Sequence=VSP_000497; InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; TYR PP.
Fam; PF00373; Band 41, 1.
Pfam; PF00595; PDZ, -5.
Ffam; PF00595; PDZ, -1.
PRINTS; PF00102; Y phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SWART; SM00295; B41; 1.
SWART; SM00194; PTPC; 1. BC039610; AAH39610.1; ALT TERM. FALSE_NEG. EMBL, U12128; AAB60339.1; -... EMBL, D21209; BAA04750.1; -... EMBL, D21210; BAA04751.1; -... EMBL, D21211; BAA04751.1; -... EMBL, X80289; CAA56563.1; -... EMBL, Z99676; CAA56124.1; -... EMBL, L34583; AAC41755.1; -... InterPro; IPR000299; Band 4.1. InterPro; IPR001478; PDZ. PROSITE; PS00660; FERM 1; FAI PROSITE; PS00661; FERM 2; FAI PROSITE; PS50057; FERM 3; 1. EMBL; L34583; AAC41755.1; -. EMBL; AF233323; AAF63474.1; EMBL; BC039610; AAH39610.1; Genew; HGNC:9646; PTPN13. 40; Conservative PIR; A54971; A54971. PIR; I67629; I67629. PIR; I67620; I67629. PDB; 3PDZ; 17-MAK-00. PDB; 1DSG; 24-JUL-02. Best Local Similarity MIM; 600267; -. Query Match Matches R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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ULAR LOCATION: Cytoplasmic (By similarity). d their effect on NF-kappaB activation."; 460:191-198(1999). Acad. Sci. U.S.A. 99:16899-16903(2002). lternative splicing; Named isoforms=4; LEOTIDE EXCHANGE FACTOR RA-GEF-2. -Q12923-1; Sequence=Displayed; 70882; PubMed=10704206; 23362; PubMed=12436199; y 39:2572-2580(2000). 0-1419 AND MET-1522 DNA sequences. e + phosphate.

43; Indels 32;

78 VNGCPEFRARATAKATVAAFAASEGHSHPR --

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MEDLINE=21143360; PubMed=11149944;

Rac1 : :: | :: | :::| | | :::| | | | :::| | | | :::| | | :::| | | | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :: 3LPKTDEGLGFNVMGG---KEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEG 165 Petersen C., Gao L., Macara I.G.; olarity protein Paré links Par3 and atypical protein kinase ated expression of atypical PKC-binding domain deleted asip human hepatocellular carcinomas."; (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
(Rel. 42, Last annotation update)
(Atypical PKC actific interacting protein) (ASIP) (CTCL tumor antigen se2-.toma, and Ovarian carcinoma;
Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
', Nagai K., Sugano S., Shiratori A., Sudo H.,
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20120; Pubmed=12234671; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sutheria; Primates; Catarrhini; Hominidae; Homo. OM N.A. (ISOFORM 5).
47023; PubMed=129897;
Noda Y., Takeuchi K., Sumimoto
novel homologue of the cell polarity protein PAR3, CEW1; QSTEW7; QSTEW7; QS6K2B; Q96RW6; Q96RW7; Q93Y57; G1648; Q9WM14; Q9NYE6; OM N.A. (ISOFORM 3), AND INTERACTION WITH PARDEB. cDNA sequencing project."; NY-2001) to the EMBL/GenBank/DDBJ databases. ophys. Res. Commun. 299:641-646(2002). OM N.A. (ISOFORMS 2; 3; 7; 8 AND 9). 20080; PubMed=11642408; 126-1356 FROM N.A. (ISOFORM 10). THKQAVETLRNTGQVVHLLL 1449 HEKAVELLKAAKDSVKLVV 186 94296; PubMed=10934474; iol. 2:531-539(2000). o tight junctions."; 313-992 FROM N.A. 1:223-229(2001). Iwayanagi T. JR3 OR PAR3A. is (Human) -99 (2002)

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Akimoto K., Izumi Y., Ohnishi T., Ohno S.;
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T. FUNCTION: Adapter protein involved in asymetrical cell divident cell Biol. 152:1183-1196(2001).
The formation of epithelial tight junctions. Association with parmosm and cell polarization processes. Seems to play a central role formation of epithelial tight junctions. Association with PARDSB may prevent the interaction of PARD3 with FIRTA/JAM1, thereby preventing tight junction assembly. The PARD5-PARD5 complex links GTP-bound Rho small GTPases to atypical proteins.
T. SUBUNIT: Interacts with PARD6A and PARD6B. Isoform 2, but results a linearacts with PARD6A or PARD6B, PRKCI similarity). Part of a complex with PARD6A or PARD6B, PRKCI similarity). Part of a complex with PARD6A or PARD6B, PRKCI similarity). Part of a complex with PARD6A or PARD6B, PRKCI similarity). Part of a complex with PARD6A or PARD6B, PRKCI similarity in the present cell-cell contact region. Colocalizes we harmony PROMITORS. Cycloplasmic; membrane associated. Par Alfrenanty PROMITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20411249; PubMed=10954424; Dahanson A.-S., Driesensm W., Aspenstroem P.; Mithe mammalian homologue of the Ceenorhabditis elegans polarity protein PAR-6 is a binding partner for the Rho GTPases Cdc42 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=3; Synonyms=C;
Isold=Q8TEM0-3; Sequence=VSP_007462, VSP_007463, VSP_0074
                                                                         Serological detection of cutaneous T-cell lymphoma-associated
Eichmueller S., Üßener D., Dummer R., Stein A., Thiel D., Schadendorf D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT OF A COMPLEX CONTAINING PARDEB AND PRKCI.
                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
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IsoId=Q8TEM0-2; Sequence=VSP_007464;
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IsoId=Q8TEW0-4; Sequence=VSP_007469;
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IsoId=Q8TEW0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
MEDLINE=21157398; PubMed=11257119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell Sci. 113:3267-3275(2000).
                                                                                                                                                                                                        SEQUENCE OF 857-1356 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH PARD6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                              antigens
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FUNCTION: Adapter protein involved in asymetrical cell diviand cell polarization processes. Plays a role in the format epithelial tight junctions. Association with PARDS may pre the interaction of PARDS with FILR/JAMI. Thereby preventing junction assembly. The PARDS-PARDS complex links GTP-bound small GTPases to atypical protein kinase C proteins. SUBUNIT: Interacts with PARDSA, PARDSB, PRKCI and PKKCZ. Pa
                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Partitioning-defective 3 homolog (PARD-3) (PARR-3) (Atypical PKC isotype-specific interacting protein) (ASIP) (Ephrin interactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20394297; PubMed=10934475;
Lin D., Edwards A.S., Fawcett J.P., Mbamalu G., Scott J.D., Paw
"A mammalian PAR-3-PAR-6 complex implicated in Cdc42/Rac1 and a
signalling and cell polarity.";
                                     STRAIN=NIH Swiss; TISSUE=Embryo;
MEDLINE=9912117; PubMed=9920925;
Lin D., Gish G.D., Songyang Z., Pawson T.;
"The carboxyl terminus of B class ephrins constitutes a PDZ dom binding motif.",
J. Biol. Chem. 274:3726-3733 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), SUBCELLULAR LOCATION, PADSPHORYLARIAN BY PRKCZ, INTERACTION WITH PRKCI AND PARD6A, SU OF A COMPLEX CONTAINING PARD6A AND CDC42, AND MUTAGENESIS OF 824-SER-SER-826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Joberty G., Petersen C., Gao L., Macara I.G.;
"The cell-polarity protein Par6 links Par3 and atypical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21828709; PubMed=11839275;
Gao L., Joberty G., Macara I.G.;
"Assembly of epithelial tight junctions is negatively regulated
                                                                                                                     SRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAK--DSVKLVV
                                                                                                                                                    491 KNILPRGAAIQDGRLKAGDRLIEVNGVDLVGKSQEEVVSLLRSTKMEGTVSLLV
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Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
"The cell polarity protein ASIP/PAR-3 directly associates with
junctional adhesion molecule (JAM).";
EMBO J. 20:3738-3748(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH PARD6B, AND SUBUNIT OF A COMPLEX CONTAINING
86 ARATAKATVAAFAASEGHSHPRV----VELPKTDEGLGFNV---
                                                                                                                                                                                                                                                                                                                              PRT; 1333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRKCI AND CDC42.
MEDLINE=20394296; PubMed≈10934474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Cell Biol. 2:531-539(2000).
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                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH FILE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein) (PHIP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to Cdc42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SROT entry is copyright. It is produced through a collaboration a Bayss Institute of Bioinformatics and the BMBL outstation a Bioinformatics Institute. There are no restrictions on its n-profit institutions as long as its content is in no way it his statement is not removed. Usage by and for commercial quires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANEOUS: Antibodies against PARD3 are present in sera from s with cutaneous T-cell lymphomas. ITY: Belongs to the PAR3 family. ITY: Contains 3 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                           =Q8TEW0-10; Sequence=VSP 007464, VSP 007465, VSP 007467, VSP_007470, VSP_007471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
Missing (in isoform 3 and isoform 5).
/FIId=VSP 007462.
                           QBTEW0-5; Sequence=VSP_007462, VSP_007463, VSP_007464, VSP_007464, VSP_007469;
                                                                                                                  -OBIEWO-6; Sequence=VSP_007463, VSP_007464, VSP_007465;
Synonyms=Lb;
                                                                                                                                                                         -QaTEW0-7; Sequence=VSP_007463, VSP_007464, VSP_007465, 
VSP_007469;
                                                                                                                                                                                                                                                                   -Q8TEW0-8; Sequence=VSP_007464, VSP_007470, VSP_007471;
                                                                                                                                                                                                                                                                                                                              VSP 007464, VSP 007465,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTS WITH PRKCZ (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tight junction; Membrane; Repeat;
on; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%; Score 167; DB 1; Length 1356; 36.0%; Pred. No. 0.00021; cive 25; Mismatches 32; Indels 16
                                                                                                                                                                                                                                                                                                                    =Q8TEW0-9; Sequence=VSP_007463, VSP_007464, VSP_007470, VSP_007471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No experimental confirmation av
SPECIFICITY: Widely expressed.
Sphorylated by PRKCZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG33676.1; ALT TERM.
AAH11711.1; ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293; AAF71530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50106; PDZ; 3.
Cell division; Tig
; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK27891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK27892.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC54037.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAA91366.1;
BAB55330.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK69192.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL76042.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL76045.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAL76046.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL76043.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAL76044.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK69193.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                       Synonyms=Sa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :16051; PARD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95; PDZ; 3.
228; PDZ; 3.
                                                                                                                                                                                                                                                                                               Synonyms=Sb;
                                                                                         Synonyms=F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671;
002;
003;
004;
005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461
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519 LAGKSQEEVVSLLRSTKMEGTVSLLVFRQEEAFHPR---EMNAEPSQMQTPKET

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PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n-profit institutions as long as its content is in no way dthis statement is not removed. Usage by and for commercial quires a license agreement (see http://www.isb-sib.ch/announce)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JPKTDEGLGFNV-----MGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JKKGTEGLGFSITSRDVTIGG---SAPIYVKNILPRGAAIQDGRLKAGDRLIEVNGVD 518
                                                                                                                                                                                                                                                                                                                                                        SPECIFICITY: All isoforms are expressed in heart, while ion in brain is mainly limited to isoform 1, and to isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                         MENTAL STACE: Isoforms 1 and isoform 3 are expressed from E E14.5, while isoform 2 is not expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Swiss Institute of Bioinformatics and the EMBL outstation Bioinformatics Institute. There are no restrictions on profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEHHEKAVELLKAAK--DSVKLVV----RYTPKVLEMEARFEKLRTARRRQQQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                 ULAR LOCATION: Cytoplasmic; membrane associated. Localize he cell-cell contact region. Colocalizes with PARD6A and
with PARD6A or PARD6B, PRKCI or PRKCZ and CDC42 or RAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION BY PRKCZ AND ABOLISHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTS WITH PRKCZ (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
KCQL -> ESGT (in isoform 3).
/FITG=VSP_007472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --
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::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tight junction; Membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMS->AMA, EME: STRONGLY REDUCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH PKRCI.
1333 AA; 149060 MW; AF67825C66DCFE86 CRC64;
                                                                                                                                                                                                                                                                          =Q99NH2-2; Sequence=VSP_007474;
Synonyms=100 kDa;
=Q99NH2-3; Sequence=VSP 007472; VSP 007473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (In isoform 2). /FIId=VSP 007474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35608; Pard3.
913; C:cell-cell adherens junction; IDA.
515; F:protein binding; IPI.
337; P:cell-cell adhesion; IC.
PR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alternative splicing.
                                                                                                                                                               lternative splicing; Named isoforms=3;
Synonyms=180 kDa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 161.5; DB 1
Pred. No. 0.00051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        007473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osphorylated by PRKCZ.
ITY: Belongs to the PAR3 family,
ITY: Contains 3 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Mismatches
                                                                                                                                                                                                                      =099NH2-1; Sequence=Displayed; Synonyms=150 kDa;
                                                                                                  c epithelial tight junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    057; AAK07669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50106; PDZ; 3.
Cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    evel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826
```

PDZ; 3

ilarity

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junction formation.",
J. Cell Sci. 115:2485-2495 (2002).

J. Cell Sci. 115:2485-2495 (2002).

J. FUNCTION: Adapter protein involved in asymetrical cell diviand cell polarization processes. Seems to play a central rothe formation of epithelial tight junctions. Association wip PARDEB may prevent the interaction of PARDS with FIIR/JAMI, thereby preventing tight junction assembly. The PARDS-PARDS complex links GTP-bound Rho small GTPasses to atypical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2; Synonyms=150 kDa;
Isold=092340-2; Sequence=VSP_007475;
TISSUE SPECIFICITY: Isoform 1 is predominently expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glandular scomech, prostate, ovary and uterus. Isoform 1 is expressed in brain, with a high expression in the cortex, hippocampus and in the striatum. Isoform 2 is predominently expressed in intestinal epithelial cells, kidney and prosta PTM: Phosphorylated by PRKCZ (By similarity). The phosphory form is concentrated at the most apical tip of cell-cell columing the initial phase of tight junction formation. SIMILARITY: Contains 3 PDZ/DHR domains.
                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Izumi Y., Hirose T., Tamai Y., Hirai S.-I., Nagashima Y., Fujim Tabuse Y., Kemphues K.J., Ohno S.; Ma atypical PKC directly associates and colocalizes at the epi tight junction with ASIP, a mammalian homologue of caenorhabdit elegans polarity protein PAR-3."; Cell Biol. 143:95-106(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinge C proteins.
SUBUNIT: Interacts with PARDGA, PARDGB and FILK/JAMI via it domain (By similarity). Interacts with PRKCI. Interacts wit (Probable). Part of a complex with PARDGA or PARDGB, PRKCI PRKCZ and CDC42 or RACI (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic; membrane associated. Loc along the cell-cell contact region. Colocalizes with PRKCZ apical edge of tight junctions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22040490; PubMed-12045219; Hirose T., Izumi Y., Nagashima Y., Tamai-Nagai Y., Kurihara H., Sakai T., Suzuki Y., Yamanaka T., Suzuki A., Mizuno K., Ohno S. "Involvement of ASIF/PAR-3 in the promotion of epithelial tight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a coberween the Swiss Institute of Bioinformatics and the EMBL of the Buropean Bioinformatics Institute. There are no restrictiuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTION WITH PRKCI AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2), SUBCELLULAR LOCATION, AND PHOSPHORYLATION OF SER-827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
                                                                           1337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9Z340-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Fibroblast;
MEDLINE=98437350; PubMed=9763423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1; Synonyms=180 kDa;
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                PARD3 OR PAR3.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                    PAD3 RAT
RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---
                                PAD3_RAT
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quires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAKATVAAFAASEGHSHPRV----VELPKTDEGLGFNV-----MGGKEQNSPIYI 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALAPPNVLSTSVGSVYNTKRVGKRLNIQLKKGTEGLGFSITSRDVTIGG---SAPIYV 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%; Score 161; DB 1; Length 1337;
.larity 31.0%; Pred. No. 0.00055;
Conservative 32; Mismatches 44; Indels 24; Gaps
                                                         549; BAA34216.1;

; T13948.

3. 3 PDZ.

BRO01478: PDZ.

288; PDZ; 3.

289; PDZ; 3.

281; PDZ; 3.

Cell division; Tight junction; Membrane; Repeat;

Phosphorylation; Alternative splicing.

271 359 PDZ 1.

461 S46 PDZ 3.

712 936 FT PDZ 3.

714 936 FT PDZ 3.

715 PDZ 3.

716 PDZ 1.

1199 1172 COLLED COLL (POTENTIAL).

1199 1172 COLLED COLL (POTENTIAL).

1199 1222 COLLED COLL (POTENTIAL).

1199 1222 COLLED COLL (POTENTIAL).

1199 1222 COLLED COLL (POTENTIAL).

1199 PROSPHORYTATION.

1034 1337 AA; 149448 MW; EC980C5106B52P9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKVLEEMEARFEKLRTARRROOO 212
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: March 18, 2004, 13:27:21

S Q18165 S QYXXH8 11 Q91XM9 Q91XM9 Q91XM9 S Q9YZZ4 S Q9YZZ 11 Q9BXY2 11 Q9BXY4 Q9YZZ4 Q9YZZ4 Q9YZZ4 Q9YZZ4 Q9YZZ4 Q9YZZ4 Q9YZZ4 Q9YZZ7 11 Q9BXY4 Q9CXIII	199.5 17.1 455 11 0952R1 199.5 17.1 455 11 095R61 198.5 17.0 454 4 0960W8 198.5 17.0 462 4 09H026 196.5 16.8 721 11 091W1 192 16.4 893 11 Q8CGN7	192 16.4 905 11 191.5 16.4 2055 11 190.5 16.3 873 13 188.5 16.1 164 11 187.5 16.0 526 11	187.5 16.0 1124 11 Q802X8 187.5 16.0 2055 11 Q804X0 187.5 16.0 2055 11 Q804X5 187.5 16.0 2055 11 Q804X5 186.5 15.9 2054 11 Q55164	185 15.8 927 11 Q62402 Q50X35 178.5 15.3 519 11 Q80TZ1 Q80	ALIGNMENTS	SULT 1 1910 014910	DT 01-0AN-1998 (TrEWBLrel. 05, Created) DT 01-MAY-1999 (TrEWBLrel. 10, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DF VELI 1 (TAX interaction protein 33) (Fragment).		L1) TISUDENCE FROM N.A. TISSUB-Testis, MEDLINE-98424246; PubMed-9753324; Butz S., Okamoto M., Sudhof T.C.;		RP SEQUENCE OF 32-233 FROM N.A. RA Rousset R., Fabre S., Desbois C., Bantignies F., Jalinot P.; RL Oncogene 15:0-0(1997). RN [3]	RP SEQUENCE FROM N.A. RA MEDILINE-9924724; bubMed=10341223; RA JO K., Derin R., Li M., Bredt D.S.; RT "Characterization of MALS/Velis-1, -2, and -3: a family of mamm. RT INN-7 homologs enriched at brain synapses in association with t RT postsynaptic density-95/NMDA receptor postsynaptic complex."; RL J. Neurosci. 19:4199-(1999).	CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN. DR BMBL; AF02825; AAC78481.1; DR BMBL; AF028826; AAB84251.1; DR BMBL; AZ73881; AAD48500.1; DR HSSP; Q12923; 3PDZ. DR Genew; HONC:17787; LIN7A.
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. tein search, using sw model	(Without alignm 1633.683 Millio 1909-005-1	BLOSUM62 Gapop 10.0 , Gapext 0.5 1017041 segs, 315518202 residues	hits satisfying chosen parameters: 1017041 ength: 0 ength: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	SPTREMBL_25:* 1: sp_archea:* 2: sp_bacter:a:* 3: sp_tung:*		9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:*	14: sp_unclassified:* 15: sp_rvirus:* 16: sp_bacteriap:* 17: sp_archeap:*	is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.	% Query Watch Length DB ID Description	233 4 014910 014910 homo 219 11 092250 zatt 211 11 092280 Q93280 Q93280 Q93280 mus	0,810.29 0,721.3 0,819.51 0,922.52 0,91A.P6 0,922.51	195 5 244 5 171 5 316 5 297 5 967 5

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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to vertebrate LIN7 homolog 1, Tax interaction protein 33
    1 MATLIVVOPLTLDRDVARAIELLEKPOESGEVPVHKLOSLKKVLOSEFCTAIREV
                                                                                                                                              ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHERAVELLKAAKDSVKLVVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEC
                                                                                                                     134 ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 EFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSP1Y1SR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 AERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEME
                                           ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.3%; Score 1057; DB 11; Length 211; 99.5%; Pred. No. 2.4e-77; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Straubberg R.;
Straubberg R.;
Straubberg R.;
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Straubberg R.;
Straubberg R.;
L. SUMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL; BC029721; AAH29721.1; -..
R WGD; WG12135609; Lin7a.
R WGC; GO:0016323; C.Da8olateral plasma membrane; IDA.
R InterPro; IPR004173; L27.
R InterPro; IPR004178; PDZ.
R PFam; PF00328; L27; 1.
R SWART; SW00269; L27; 1.
R SWART; SW00269; L27; 1.
R SWART; SW00269; DZ7; 1.
R PFAM; PF00595; PDZ; 1.
R SWART; SW00269; PDZ; 1.
R SWART; SW00269; DZ7; 1.
R SWART; SW00269; DZ7; 1.
R SWART; SW00269; DZ7; 1.
T NOW IER 1.
SEQÜENCE 211 AA; 23752 WW; 73ADE354FC8BEE83 CRC64;
                                                                                                                                                                                                                               EEMEARFEKLRTARRRQQQQLLI-QQQQQQQQQQQQQNHMS 219
                                                                                                                                                                                                  194 EEMEARFEKLRTARRROOQQLLICOQQQQQQQQQUHMS 233
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Best Local Similarity 99.55
Matches 210; Conservative
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                                         74
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Q9NUP9;
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Q8JZS0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
tiheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;
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is elegans lin-7: localization at cell-cell junctions.";
2811-2817(1999).
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19097; Pubwed=10362251;
a Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka
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                                                                                                                                                                                                                                                        100.0%; Score 1170; DB 4; Length 233; 100.0%; Pred. No. 2.2e-86; ive 0; Mismatches 0; Indels 0;
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R004172; L27.
R001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; L27; 1.
15; PDZ; 1.
128; PDZ; 1.
128; PDZ; 1.
1010; PDZ; 1.
119 AA; 24549 MW; 6EB6AAAPCSCIEC74 CRC64;
                                                                                                                                                                                                                   33 AA; 25997 MW; D8D05EF16A93BE7B CRC64;
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
15; F:protein binding; IPI.
187; P:exocytosis; TAS.
181; P:protein complex assembly; TAS.
180:04172; L27.
180:L27; 1.
181; L27; 1.
184; PDZ, 1.
185; PDZ, 1.
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                                                                                                                                                                             0106; PDZ; 1.
                                                                                                                                                                                                                                                                                                 Conservative
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LIN7C OR VELI3 OR MALS-3.
                                                                                                                           201 EKLRTARROO 211
                                                                                                                                                         186 EKMRSAKRROO 196
                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse),
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D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
L., Gozes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
W., Touchman J.W., Green E.D., Dickson M.C.,
C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
Marra M.A.,
Marra M.A.,
Marra M.A.,
Marra M.A.,
Man and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                      Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
, Nagai K., Sugano S., Shiratori A., Sudo H.,
, Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
, Chiba Y., Inda S., Murakawa K., Ono Y., Takiguchi S.,
, Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
, Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
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                                                l protein FLJ11215 (LIN/L process).
8 (Human).
Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; utheria; Primates; Catarrhini; Hominidae; Homo.
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; Pred. No. 8.5e-58;
24; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                  cDNA sequencing project."; FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JUN-2003) to the EMBL/GenBank/DDBJ databases.
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PR004172; L27.
PR001478; PDZ.
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                  (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 25, Last annotation update) protein FLJ11215 (LIN7C protein).
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(TrEMBLrel. 15, (TrEMBLrel. 15,
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:17789; LIN7C
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197 AA; 2:
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0.1-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to lin 7 homolog c (C. elegans).
Xenopus laevis (African clawed frog).
Xenopus haevis (African Clawed frog).
Assaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostom Amphibia; Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98424246; PubMed=9753324;
MEDLINE-98424246; PubMed=9753324;
MEDLINE-98424246; PubMed=9753324;
MEDLINE-98424246; PubMed=9753324;
"A tripartite protein complex with the potential to couple syna;
"A tripartite protein complex with the potential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostom.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; M.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 VVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 PGGIADRHOGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAQGKVKLVVRYTPRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 PGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 NGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 SSSPEVRANATAKATVAAFAASEGHSHPRVVELPKTEEGLGFNIMGGKEQNSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.4%; Score 812; DB 13; Length 197; 79.8%; Pred. No. 1.2e-57; Live 25; Mismatches 14; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S., Sträusberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC01249; AA141249.1; -.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VELI 2 (Vertebrate homolog of C. elegans Lin-7 type 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50106; PDZ; 1.
197 Aa; 21889 MW; F25EEF4A1219E87A CRC64;
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                                                                                                                                                   197 AA.
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184 RFEKMRSAKRRQQ 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 RFEKLRTARROO 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarry .... Matches 154; Conservative
                                                                                                                                                 PRELIMINARY;
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                                            186 EKMRSAKRRÓG 196
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    201 EKLRTARROQ 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02828; L27; 1.
Pfam; PF00595; PDZ; 1.
SMART; SM00569; L27; 1.
SMART; SM00228; PDZ; 1.
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SEQUENCE 197 AA; 218
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                     Q7ZYU3;
                                                                                                                                                 Q7ZYU3
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088951
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J., Collins F.S., Wagner L., Shenmen C.M., Schnier G.D.,

F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

J.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

K., Marny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

alton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

W., Touchman J.W., Green E.D., Dickson M.C.,

C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Marra M.A., Schaltz J., Myers R.M., Butterfield Y.S.,

Marra M.J., Schaltz J., Myers R.M., Schein J.E.,

Marra M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRANATAKATVAAFAASEGHSHPRVVELPKTEEGLGFNIMGGKEQNSPIYISRIIPG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JILDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anome Exploration Research Group Phase I & II Team; E the mouse transcriptome based on functional annotation of Jength cDNAs."; 665-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
\Upsilon , annotation of a full-length mouse cDNA collection.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.; 38B-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10839; Lin7c.
242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 AA; 21834 MW; 7410FBFA3BD24F45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:16899-16903 (2002).
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live 24; Mismatches 13
                                                                                                     se; STRAIN=C57BL/6J; TISSUE=Cecum; 54683; PubMed=12466851;
                                                                                                                                                                                                                                                                    OM N.A.
se; TISSUE=Eye;
38257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595; AAC78483.1; -. 136; AAC78075.1; -.
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se; TISSUE=Eye;
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PR004172; L27.
PR001478; PDZ.
                                         585-690(2001).
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Acad. Sci. U.
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                                                                                                                                             Consortium,
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TISSUB-Kidney;
Olsen O., Liu H., Merot J., Welling P.A.;
"Basolateral Membrane Expression of the Kir 2.3 Channel is Coor by a PDZ Interaction with Lin-7/CASK.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      74 BIIIVNGCPEFRARATAKAIVAAFAASEGHSHPRVVELPKIDEGLGFNVMGGKE
                                                                                                                                                                                                                                                                                                                             119 ISRVIPGGVADRHGGLKRGDQLLSVNGVSVBGEHHEKAVELLKAAQGSVKLVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostom
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 MATLIVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIRE
                                                                                                                                                                                                                                14 MATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIRE
                                                                                                                                                                                                                                                                                                                                                                       134 ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Lin-7D protein, likely ortholog of mouse LIN-7B, mammalian LIN-
                                                                                                                                                                                                 3
                                                                                                                                                           69.1%; Score 809; DB 11; Length 207; 79.3%; Pred. No. 2.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.0%; Score 807; DB 4; Length 207; Best Local Similarity 78.5%; Pred. No. 3.3e-57; Matches 157; Conservative 24; Mismatches 17; Indels
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0007242; P:intracellular signaling cascade; IEA.
InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
                                                                                                                            BC6B6754B8C89B13 CRC64;
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                                                                                                                                                                                                 15;
                                                                                                                                                                           79.3%; Pred. No. 2.3e-
tive 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           194 EEMEARFEKLRTARRROQ 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22900 MW;
InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
Pfam; PF02828; L27; 1.
Pfam; PF00595; PDZ; 1.
SMART; SM00569; L27; 1.
RNO17E; SM00228; PDZ; 1.
RNO17E; PS05116; PDZ; 1.
SEQUENCE 207 AA; 222900 b
                                                                                                                                                                             Best Local Similarity 79.33
Matches 157; Conservative
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Pfam; PF00595; PDZ; 1.
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Best Local S
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     SORRERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n R., Li M., Bredt D.S., zation of MALS/Velis-1, -2, and -3: a family of mammalian ogs enriched at brain synapses in association with the c density-95/NMDA receptor postsynaptic complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agicus (Rat).
Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Ltherla, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and characterization of mammalian homologues of
tis elegans lin-7: localization at cell-cell junctions.";
:2811-2817(1999).
ITY: COWTAINS 1 PDZ/DHR DOMAIN.
133; AAC78072.1; -.
3; 3PDZ.
242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM N.A.
89097; PubMed=10362251;
ta Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.1%; Score 809; DB 11; Length 207; 79.3%; Pred. No. 2.3e-57; ive 24; Mismatches 15; Indels ;
                                                                                                                                                                                                                                             JUN-2002) to the EMBL/GenBank/DDBJ databases.
94; AAC78482.1; ".
082; AAD48501.1; ".
780; AAH31780.1; -:
                                                                                                                                                                                                                                                                                                                                                                                                                                       50106; PDZ; 1.
207 AA; 22914 MW; BC6B6754B8C89F03 CRC64;
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Last annotation update)
cytosis to cell adhesion in brain.";
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                                                                                                                                                                                                                                                                                                               3; 3PDZ.
30858; Lin7b.
886; C:plasma membrane; IDA.
PRO04172; LZZ.
PRO01478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last seq.
(TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                   74724; PubMed=10341223;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S. Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H.C., Blazel R.G., Champen M., Hedderson S. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Randon R.C., Rogers Y.H.C., Blazel R.G., Champen M., Pietiffer I. Baraten B. B. Barten B. B. Brottier P., Bartil J.F., Agbayani A., Barten B. B., Bhadari D., Botchan M.R., Bouck J., Bradari D., Botcher M., Gawley S., Ballek C., Bradari B. B., Canley S., Barten B. B., Darles B., Dalike C., Dankova D., Botchan M.R., Bouck J., Bayenott L.B., Davies P., Botchy J., Cawley S., Dalike C., Davenport L.B., Davies P., Botchon K., Doup L.E., Downes M., Dugan-Rocha S., Dankov B. B.C., D. Duthin K.J., Evangeliara C.C., Ferraz C., Ferriera S., Fleischm Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K. Botchu K.J., Harvey D., Healman T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchu Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z. Liang Y., Lin X., Mattei B.M., Murphy B., Murphy D., Murzhy D.M., Nelson D., Nelson D., Nelson D., Nelson D., Nelson D., Nelson D., Nelson E., Siden-Kiamos I., Simpson M., Stupski M.P., Shu E. Spradling A.C., Stapheton M., Stupski M.P., Shu E. S., Siden-Kiamos I., Stupsko M., Shu B., Shu B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 SHDVRASATAKATVAAFAASEGHAHPRVVELPKTEEGIGFIVVMGGKEQNSPIYI!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 QPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 CPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYI
                         Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidas; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.4%; Score 754; DB 5; Length 19577.9%; Pred. No. 5.8e-53; ive 20; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0039269; veli.
GO: GO:0007242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21493 MW; EF9DFSED71A73FBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003750; AAF56389.1;
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InterPro; IPR001478; PDZ.
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Pfam; PF00595; PDZ; 1.
SMART; SM00569; L27; 1.
SMART; SM00228; PDZ; 1.
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SEQUENCE 195 AA; 21
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                                                                                                                                                                SEQUENCE
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Matches
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                                                                                 CDITGSAEIRAHATAKATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKEQNSPIY 118
                                                                                                                                  RIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
                                                                                                                                                              TVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY 120
                                              ITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LIVVQPLTLDRDVARAIBLLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 73
AL--VEPLGLERDVSRAVELLERLQRSGELPPQKLQALQRVLQSRFCSAIREVYEQLY 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   egicus (Rat).
Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Atheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and characterization of mammalian homologues of is elegans lin-7: localization at cell-cell junctions."; [TY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM N.A.
19097; PubMed=10362251;
:a Y., Deguchi M., Ide N., Hirao K., Yao I., Nishioka H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .82 AA; 19927 MW; D448E3BBCF5A51DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIIPGGVAERHGGLKRGDQLLSVNGVALE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AA.
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                                                                                                                                                                                                                                                       TEARFEKLRTARROOOO 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134; AAC78073.1; -.
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3; 3PDZ.

.0116;

LRTARRQ 210 QRNTRRRO 195

244 AA. PRT; PRELIMINARY;

(TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 24, Last annotation update) Created) (TrEMBLrel. 23, (TrEMBLrel. 23,

melanogaster (Fruit fly). Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota; Motoperygota; Diptera; Brachycera; Muscomorpha; , Drosophilidae; Drosophila.

Occopies PubMed=10731132;
Occopies S.E., Holt R.A., Evans C.A., Goccayne J.D.,
P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,
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Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
Moy M., Murphy B., Murphy L., Moris J., Woshrefi A.,
Nelson K.A., Nixon K., Nusskern D.R., Parl W., Reee M.G.,
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Tector C., Turner R., Venter E., Wang A.H., Wang X.,
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Wyers B.W., Rubin G.M., Venter E.,
Bernence of Drospohila M., Zhou X., Zhu X., Zhu X., Smith H.O.,
Wyers B.W., Rubin G.M., Venter E.,

E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Center A., Champe M., Davenport L.B., Dietz S.M., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Frise E., Galle R.F., Garg N.S., George R.A.,

Drosophila melanogaster.";

2185-2195 (2000)

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SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbel Misra S., Crosby M.A., Kaminker J.S., Prochnik S.E., Smith C.D.

Tupy J.L., Bergan C., Berman B., Carlson J.W., Celniker S.E., Clamp J.L., Bergan C., Emmert D., Frise B., de Grey A., Harris Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Mitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.; "Annotation of Drosophila melanogaster genome."; Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases. Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McHucosh T.C., Moy W., Murphy B., Nelson C., Nelson K.A., Nunoc Pacleb J., Paragas V., Park S., Patel S., Pétiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M. "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. 6 EPLTLSRDVKRSIELLEKLQASGDFPTTKLAALQKVLNSDFMTSVREVYEHVYE 53; 21 OPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHE 117 ------BLGFNVMGGKEQNSPIYISRIIPGGVA 126 KVYRPRIYVSIIHLIWKALSIFNFCFSGLGFNVMGGKEQNSPIYISRIIPGGVA 150 KRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKL 186 KRGDQLLSVNG--VVRENHEKAVELLKQAVGSVKLVVRYTPKVLEEMEMRFDKQ 58.5%; Score 684.5; DB 5; Length 244; 59.8%; Pred. No. 3.1e-47; ive 20; Mismatches 24; Indels 53; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE003750; AAN14038.1; -. FlyBase; FBqn0039269; veli.
FlyBase; FBqn0039269; veli.
Occopy GO:000742; Pintracellular signaling cascade; IEA.
InterPro; IRR004172; L27.
InterPro; IPR001478; PDZ. 27467 MW; 0A464B355772ABA1 CRC64; 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-CTr-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein (Fragment). 81 CPEFRARATAKATVAAFAASEGHSHPRVVELPKTDE-Matches 144; Conservative PRELIMINARY; Pfam; PF02828; L27; 1.
Pfam; PF00595; PDZ; 1.
SMART; SM00569; L27; 1.
SMART; SM00228; PDZ; 1. PROSITE; PS50106; PDZ; 244 AA; Best Local Similarity SEQUENCE FROM N.A. SEQUENCE FROM N.A. 210 Q 210 244 0 244 SEQUENCE Query Match 017458; 017458 RESULT 13 017458 ID 017458 AC 01 DT 01 DT 01 ð d à q ₽ g δ 셤 ò

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditod
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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MEDLINES-6200711, PubMed-8612272;
Simske J.S., Kaech S.M., Harp S.A., Kim S.K.;
"LET-23 receptor localization by the cell junction protein LIN-7.
                                                                                                                                                                                                                                            25 LDRDVARAIBLLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVN
                                                                                                                                                                                                                                                                                                                                         237 RHGGLKRGDQLIAVNG-NVEAECHEKAVDLLKSAVGSVKLVIRYMPKLLDEMERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 LDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 RARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIF
                                                                                                                                                                                                                                                                             117 LERDVORILELMEHVOXTGEVNNAKLASLOOVLOSEFFGAVREVYETVYESIDAI
                                                                                                                                                                                                                                                                                                                    85 RARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRII!
                                                                                                                                                                                                                                                                                                                                                                                            145 RHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 316;
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                                                                                                                                                               Query Match 55.3%; Score 647.5; DB 5; Length 3 Best Local Similarity 67.9%; Pred. No. 4.1e-44; Matches 129; Conservative 30; Mismatches 30; Indels
InterPro; IPR004172; L27.
InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
Pfam; PP00228; L27; 1.
SMART; SM00259; L27; 1.
SMART; SM00228; D27; 1.
SMART; SM00228; PDZ; 1.
SROSTIE: PS50106; PDZ; 1.
SEQUENCE 316 AA; 35663 MW; E050959F2D29BBFF CRC64;
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InterPro; IPR004172; L27.
InterPro; IPR001478; PDZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
EMBL; U78092; AAB36684.1; -.
HSSP; Q12959; 1PDR.
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Cell 85:195-204(1996).
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NON TER 297 297
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Pfam; PF00595; PDZ; 1.
SMART; SM00569; L27; 1.
SMART; SMO0228; PDZ; 1.
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P90976;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHKLQSLKKVLQSEFCTAIREVYQYMHETITVNGCPEFRARATAKAIVAAFAASEGH 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Joulson P.S., Wilson R.A.;
aation, cloning and immunogenicity of antigens released by
tarvae of Schistosoma mansoni.";
tarvae of Schistosoma mansoni.";
(Tr. CONTALNS 1 PDZ/DHR DOMAIN.
### FORT PDZ/DHR DOMAIN.
### FORT PDZ/DHR DOMAIN.
                   Metazoa, Platyhelminthes, Trematoda, Digenea, Strigeidida, oidea, Schistosomatidae, Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       letazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLRTARRQ 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ); 1PDR.
:G11A.10; CE28370.
:42; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                      342; P:intracellular signaling cascade; IEA. R004172; L27. R001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AA; 19000 MW; 69685F4108598063 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.4%; Score 648.5; DB 5; 73.7%; Pred. No. 1.5e-44; tive 26; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TY: CONTAINS 1 PDZ/DHR DOMAIN.
188; CAA22459.2; -
                                                                                                                              14538; PubMed=10406037;
 mansoni (Blood fluke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ig biology.";
2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                  28; 127; 1.
35; PDZ; 1.
228; PDZ; 1.
30106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                         OM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       larity
                                                                                                                                                                                                                                                              1BFE.
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AATAKATVAAFAAAEGHAHPRIVELPKIDQGLGFNVMGGKEQNSPIYISRIIPGGVAD 236

GGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204

: March 18, 2004, 13:28:20 cs

1 į

26 807 69.0 207 7 ADB83812 Adb83812 27 807 69.0 207 7 ADB872967 Adb72267 28 807 69.0 207 7 ADG36805 Adc36805 29 807 69.0 207 7 ADG27895 Adc31095	807 69.0 207 7 ADC49826 807 69.0 207 7 ADC49925	807 69.0 207 7 ADC495942 807 69.0 207 7 ADC47148 807 69.0 207 7 ADC77148	807 69.0 207 7 ADD06258 807 69.0 207 7 ADC77777 807 69.0 207 7 ADD56740	807 69.0 207 7 ADD50986	807 69.0 207 7	807 69.0 207 8 ADC48779	807 69.0 207 8 ADE05794	ALIGNMENTS	RESULT 1 AAY29978 ID AAY29978 standard; protein; 233 AA.	AAY29978;	23-NOV-1999 (first entry)	Human cell junction PDZ protein CJPDZ.	<pre>Human; cell junction PDZ protein; PDZ domain; CJPDZ; diagnosis; neurological disorder; developmental disorder; William's syndrc</pre>	Homo sapiens.	US5958731-A.	28-SEP-1999.	11-SEP-1998; 98US-00151611.	11-SEP-1998; 98US-00151611.	(INCY-) INCYTE PHARM INC.	Yue H, Patterson C, Au-Young J;		WPI; 1999-561035/47. N-PSDB; AAZ21259.	ır junction PDZ protein	the prevention, diagnosis and treatment of disorders associated defective cell signaling such as cancers and neurological and	disorders.	Claim 1; Col 39-40; 27pp; English.	The present sequence represents human cell junction PDZ protein	CJPDZ polynucleotides and proteins may be used in the diagnosis prevention and treatment of disorders associated with defective	signalling. They may be used to treat cancers, neurological dis developmental disorders such as William's syndrome. C1PDZ or ve	containing COIDS may be administered to treat any the above by rectifying mutations or deletions in a matient's conome that	cell signalling by expressing inactive proteins or to supplemen	patients own production of CJPD2 protein domains. Antisense nuc molecules may be administered to down regulate CJPD2 protein do expression by binding with the cells own CJPD2 genes and preven	
					-				REST AAY	X X X	4 日 3	¥ 晋 \$	X E E X	SO	883	¥ &	XX FG	XX PR	X &	X Id	XX	# H H	* E	F	Ld.	PS	8 8	88	88	388	388		
.6 pugen Ltd.		h time 59 Seconds tout alignments) 823 Million cell updates/sec		LLIQQQQQQQQQQQQQQNHMS 233			;: 1586107							ם מזיבל ריז מיחבלה זע לה	of the result being printed, one distribution	ore discribation:		Description	Human	Aau07127 Human cel Aau99326 Human cel	Human	Human	Human	Aae03655 Human ext Aau83629 Human PRO		Novel Human	Human	Human Human	Novel Novel		Human	AGD/8049 NOVEL DUM AGD87115 Human PRO AGD84697 Human PRO	
GenCore version 5.1. Copyright (c) 1993 - 2004 Comp	tein search, using sw model	March 18, 2004, 13:19:49; Search time (without ali	US-09-909-005-1 1170	MLKPSVTSAPTADMATLTVV	BLOSUM62 Gapop 10.0 , Gapext 0.5	1586107 seqs, 282547505 residues	hits satisfying chosen parameters	ength: 0 ength: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	κt'.			s: geneseqpzousas:* 7: geneseqpzousas:* 8: geneseqpzousas:* 9: qeneseqpzousas:*	s the mimber of results predict	er than or equal to the score of	analysis of the total so	SUMMARIES	Query Match Length DB ID	.0 233 2	.0 233 4	.0 233 7	7.0 233 / 9.6 197 4	9.6 198 4	9.0 207 4	3.0 207 6	207 6	9.0 207 6	9.0 207 7	9.0 207 7 9.0 207 7	7 702 0.6	7 702 0	69.0 207 7 ADB87115 69.0 207 7 ADB87115 69.0 207 7 ADB84697	

ij CUPDZ polynucleotides may also be used as DNA probes in assays to detect and quantitate the presence of similar l sequences in samples, and hence which patients may be in orative therapy. They may also be used to study the and function of CUPDZ protein domains and their role in ghalling. The CUPDZ protein domains may be used as antigens ion of antibodies and in assays to identify modulators of ssion and activity

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                                                                                                                                                                                                            120
                                                                                                                                                                                                                                              AIRBVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGF 120
                                                                                                                                                                                                                                                                                                        GGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD 180
                                                                                                                                                                                                                                                                                                                                             GGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD 180
                                                                                                       9
                                                                                                                                                 CPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLÕESGEVPVHKLÕSLKKVLÕSE 60
                                                                                                    PSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVTQSE
                                                                                                                                                                                                      AIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGF
                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             LVVRYTPKVLEEMEARFEKLRTARRROOOLLIQOOOOOOOOOOOTOONHMS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1170; DB 2; Length 233;
; Pred. No. 7.5e-108;
0; Mismatches 0; Indels 0;
     100.0%;
                                                  Conservative
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ndard; protein; 233 AA.

(first entry)

unction PDZ protein, CJPDZ.

junction PDZ protein; CJPDZ; antigen; antibody; cytostatic; itc; neuroprotective; antibplieptic; anti-Alzheimer's disease; nti-convulsant; cancer; leukaemia; myeloma; sarcoma; disorder; epilepsy; Alzheimer's disease;

Location/Qualifiers 107. .189 /label= PDZ_domain

99US-00370102.

98US-00151611.

TE GENOMICS INC.

Patterson C; oung J,

107. .189 /note= "Putative PDZ domain"

3943/50.

ction PDZ proteins useful in the prevention, diagnosis and disorders associated with defective cell signaling such as urological disorders and developmental disorders such as ndrome.

18-JUL-2001; 2001US-00909005.

US2002082388-A1.

Domain

27-JUN-2002

98US-00151611

11-SEP-1998;

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The invention relates to a purified human cell junction PDZ (CJJ polypeptide. The polypeptide may be used as an antigen in the profamiliar throaties against CUPDZ and in assays to identify molecules bind CJPDZ including modulators of CIPDZ expression and activity antibodies including modulators of CIPDZ expression and activity of CMPDZ. The anti-CJPPZ entibodies may also be used as diagnostic agents for detecting the presence of CJPDZ polypeptides in samples (e.g. by enzyme linked immunoabsorbant assay, ELISA). Disorders of cell signalling and expression and activity that may be prevented, diagnosed and/or by the above methods include, for example cancers (e.g. leukaem: myeloma, sarcoma or lung, liver, colon or spleen cancer), neurol chiscoders (e.g. epilepsy, Alzheimer's disease and/or Huntington chorea). A full list of disorders that may be treated is given is specification. The present sequence represents human CJPDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytostatic, nootropic, neuroprotective, endocrine, cell junction PDZ: CJPDZ; membrane-associated signalling protein ginal transduction, postsynamptic density protein 95; PSD-95; Drosophila lethal (1) discs large-1; DIg; zonula occludens-1; ZC cell signalling; cancer, leukaemia, lymphoma; neurological disci Alzheimer's disease; Parkinson's disease; developmental disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FCTAIREVYQYMHETIIVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVKLVVRYTPKVLEEMEARFEKLRTARRRQQQQLIQQQQQQQQQQNHMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVKLVVRYTPKVLEEMEARFEKLRTARRROOOOLLIQOOOOOOOOOOOHMS
                                                                                                                                                                                                                                                                                                                                                                                                             Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1170; DB 4; 100.0%; Pred. No. 7.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cell junction PDZ (CJPDZ) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       muscular dystrophy; William's syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ŗ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU99326 standard; protein; 233
                  Claim 1; Fig 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                       Sequence 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU99326;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
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99US-00370102.

TE PHARM INC.

ပ် Patterson oung J,

7135/57.

nction PDZ protein domains useful in the prevention, diagnosis it of disorders associated with defective cell signaling such neurological disorders and developmental disorders such as

3 1; 31pp; English.

un discloses a human cell junction PDZ (CJPDZ) polypeptide and leotide encoding it. PDZ is a conserved protein domain which led in various membrane-associated signalling proteins. These uple activated receptors to downstream second messenger play a key role in the regulation and coordination of Lipprotein signal transduction pathways. PDZ domains were the three proteins they were first identified in . . density protein 95 (PSD-95), Drosophila lethal (1) discs j) and zoula occludens. 1 (20-1). The polypeptides and ides can be used to diagnose or treat a disease or condition with decreased expression of functional CJPDZ, for screening or effectiveness as agonists or antagonists, for screening at modulates the protein activity, for screening compounds in altering gene expression and for raising antibodies. liam's syndrome). ides and polynucleotides are useful for the prevention, in treatment of disorders associated with defective cell such as cancers (e.g. leukaemia and lymphoma), neurological 9.g. Alzheimer's disease and Parkinson's disease) and il disorders (e.g. muscular dystrophy and William's syndrome presented is the human cell junction PDZ (CJPDZ) protein

Gaps 0; DB 5; Length 233; 0; Indels 100.0%; Score 1170; DB 5; 100.0%; Pred. No. 7.5e-108; Mismatches 0; Conservative larity

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09 09 CPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSE CPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSE 120 120 PAIREVYOYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGF AIREVYOYMHETIIVNGCPEFRARATAKAIVAAFAASEGHSHPRVVELPKTDEGLGF AGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD 180 IGGKEQNSPIYISRIIPGGVAERHGGIKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD

CLVVRYTPKVLEEMEARFEKLRTARRRQQQQLLIQQQQQQQQQQQQDHMS 233 CLVVRYTPKVLEEMEARFEKLRTARRRQQQQLLIQQQQQQQQQQQQUHMS 233

andard; protein; 233 AA.

(first entry)

in NP 004655, SEQ ID NO 12387.

; neuronal tissue; gene therapy; ental nerve injury; chronic constriction injury; CCI; e injury; SNI; Chung.

ftp.wipo.int/pub/published_pct_sequences. Befort K, Claim 1; Page; 1017pp; English. 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765 (GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG. Matches 233; Conservative Woolf C, D'urso D, WPI; 2003-268312/26. Local Similarity GENBANK; NP 004655 Sequence 233 AA; WO2003016475-A2. Homo sapiens. 27-FEB-2003 Query Match Best Local S

.. 0 Length 233; Indels 100.0%; Score 1170; DB 7; 100.0%; Pred. No. 7.5e-108; 0; Mismatches 1 MIKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLK 1 MLKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLK

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61 FCTAIREVYQYMHETIITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKT 61 FCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKT ð

121 NVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVEL 121 NVMGGKEONSPIYISRIIPGGVAERHGGLKRGDOLLSVNGVSVEGEHHEKAVEL à 임

181 SVKLVVRYTPKVLEEMEARFEKLRTARRRQQQQLLIQQQQQQQQQQQUHMS

à

Costigan M;

New composition comprising two or more isolated polypeptides, preparing a medicament for treating pain in an animal.

expressed in an animal subjected to pain, a method for identify compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical compose activity in an animal of one or more of the polympetides given activity in an animal of one or more of the polympetides given a specification, a method for identifying a compound useful in tropin and a pharmaceutical composition comprising the one or more oplympetides or their antibodies. The polymucleotide or the composition and a pharmaceutical composition comprising the one or more polympetides or their antibodies. The polymucleotide or the commodulates its activity is useful for preparing a medicament for pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. therapy). The sequence presented is a human protein (shown in T therapy). The sequence presented is a human protein (shown in T the sequence data for this patent did not form part of the prin specification, but was obtained in electronic form directly fro The invention discloses a composition comprising two or more issor thuman polymucleotides or a polymucleotide which represents a derivative or allelic variation of the nucleic acid sequence. A claimed are a vector comprising the novel polymucleotide, a hos comprising the vector, a method for identifying a nucleotide sewich is differentially regulated in an animal subjected to pai kit to perform the method, an array, a method for identifying a that increases or decreases the expression of the polymucleotid subjected to pain, a method for identifying a compound which return the expression of a polymucleotide sequence which is differential

TUVRYTPRVLEEMEARFEKLRTARRRQQQULLIQQQQQQQQQQQHHMS 233

indard; protein; 233 AA.

(first entry)

in NP_004655, SEQ ID NO 1207.

; neuronal tissue; gene therapy; antal nerve injury; chronic constriction injury; CCI; a injury; SNI; Chung.

5-A2.

2002WO-US025765.

2001US-0312147P. 2001US-0346382P. 2001US-0333347P.

HOSPITAL CORP.

R AG.

Costigan M; Befort K, urso D,

8312/26. 004655. ion comprising two or more isolated polypeptides, useful for medicament for treating pain in an animal.

e; 1017pp; English.

a vector comprising the nevel polymucleotide, a host cell he vector comprising the nevel polymucleotide, a host cell he vector, a method for identifying a nucleotide sequence ferentially regulated in an animal subjected to pain and a time the method, an array, a method for identifying an agent esentially expressed in neuronal tissus of a first animal pain, a method for identifying a compound which regulates on of a polynucleotide sequence which is differentially a natural subjected to pain, a method for identifying a compound which regulates on of a polynucleotide sequence which is differentially a natural subjected to pain, a method for identifying a tregulates the activity of one or more of the dest a method for method for method for identifying a compound useful in treating harmaceutical composition, a dentifying a compound or small molecule that regulates the an animal of one or more of the polypeptides given in the in, a method for identifying a compound useful in treating harmaceutical composition comprising the one or more of the polymucleotide or the compound that sameceutical merve injury (chung), chronic constriction and spared nerve injury ((hung), chronic constriction in the was obtained in electronic form directly from WIPO at (pub)/published_pot_sequences. on discloses a composition comprising two or more isolated rat-ynucleotides or a polynucleotide which represents a fragment, or allelic variation of the nucleic acid sequence. Also

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1 MLKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKO
                                                                                                                                      1 MLKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLK
                                                                                                                                                                                           61 FCTAIREVYOYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKT
                                                                                                                                                                                                                                                                                       121 NVMGGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVBGBHHEKAVEL;
                                                                                                                                                                                                                                                                                                                                     121 NVMGGKEQNSPIYISRIIPGGVABRHGGLKRGDQLLSVNGVSVEGEHHEKAVELJ
                                                                                                                                                                                                                                            61 FCTAIREVYQYMHETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKT
                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                       181 SVKLVVRYTPKVLEEMEARFEKLRTARRRQQQQLLIQQQQQQQQQQQQUHMS
  Length 233;
                                                  0; Indels
100.0%; Score 1170; DB 7;
100.0%; Pred. No. 7.5e-108;
ive 0; Mismatches 0;
Ouery Match
Best Local Similarity 100.
Matches 233; Conservative
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AAM78892 standard; protein; 197 AA.

AAM78892;

06-NOV-2001 (first entry)

Human protein SEQ ID NO 1554.

Human, cytokine, cell proliferation, cell differentiation, gene vaccine; peptide therapy, stem cell growth factor; haematopolesi tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.

Homo sapiens.

WO200157190-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US004098

2000US-00496914 2000US-00598075

2000US-00620325 2000US-00654936

2000US-00663561. 2000US-00693325. 2000US-00728422. 03-FEB-2000; 27-APR-2000; 20-JUN-2000; 219-JUL-2000; 215-SEP-2000; 20-CT-2000; 2

(HYSE-) HYSEQ INC

¥.7 Cao Drmanac RT, Asundi V, Zhou P, Xu C, Wang D, Wang J, Zhang J, Ren F, Chen Wejhrman T, Goodrich R; Tang YT, Liu C, Drmanac RT, Ma Y, Zhao QA, Wang D, Wang Xue AJ, Yang Y, Wejhrman T,

WPI; 2001-476283/51. N-PSDB; AAK52025.

Nucleic acids encoding polypeptides with cytokine-like activitie in diagnosis and gene therapy

Claim 20; Page 3872-3873; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and encoded polypeptides (AAM78323-AAM80302) that exhibit activity e cytokine, cell proliferation or cell differentiation or which ma production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vac peptide therapy. The polypeptides have various cytokine-like act

Sequence 197 AA; WO200157190-A2. Homo sapiens. 03-FEB-2000; 27-APR-2000; 20-JUN-2000; 19-JUL-2000; 01-SEP-2000; 15-SEP-2000; 06-NOV-2001 09-AUG-2001 201 AAM79876; Query Match **AAM**79876 RESULT 888888888888888888888888888888888888 g ð à g A CONTRACTOR OF THE CONTRACTOR Š o, ell growth factor activity, haematopoiesis regulating issue growth factor activity, immunomodulatory activity and ibin activity and may be useful in the diagnosis and/or f. cancer, leukaemia, nervous system disorders, archritis and n. Note: Records for SRQ ID NO 2110 (AAK2281), 2111 and 3666 (AAM80020) are omitted as the relevant pages from the sting were missing at the time of publication 140 SVRANATAKATVAAFAASEGHSHPRVVELPKTEEGLGFNIMGGKEQNSPIYISRIIPG 125 for synthesizing polynucleotides, particularly the 5602 full-defined in the specification, and for the detection and/or the abnormality of the proteins encoded by the full-length UTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHRTITVNG 80 VRLERDICRAIELLEKIQRSGEVPPOKIQALQRVIQSEFCNAVREVYEHVYETVDISS 65 invention describes primer sets for synthesising 5602 full-3 defined in the specification. Where a primer set comprises: SFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPG AERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARF Gaps er; detection; diagnosis; antisense therapy; gene therapy. Yamamoto J; ;) ID NO 13038; 2537pp + Sequence Listing; English. Length 197; ; Score 814; DB 4; Length 197; Pred. No. 1.6e-72; 24; Mismatches 13; Indels nikawa T, Hayashi K, Saito K, Yi Wakamatsu A, Nagai K, Otsuki T; in sequence SEQ ID NO:13038. indard; protein; 197 AA. Nishikawa T, 99JP-00300253. 2000JP-00118776. 2000JP-00183767. 69.6%; ; 2000EP-00116126. 99JP-00248036. 2000JP-00241899 (first entry) Conservative :|:|:|||||| MRSAKRRQQ 196 RTARREQ 211 yai T, Nish Igiyama T, X RES INST. 7 AA;

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(a) an oligo-dT primer and an oligonucleotide complementary to complementary strand of a polymucleotide which comprises one of nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a com of an oligonucleotide comprising a sequence complementary to the complementary strand of a polymucleotide which comprises a 5-b sequence and an oligonucleotide comprises a 3-b and sequence, where the oligonucleotide which comprises a 3-b and sequence, where the oligonucleotide comprises a 1-bast 15 nucleotides and the complete 5'-end sequence/3'-end sequence is selected from those defi
                                                                                                                                                                                                                                                                                                                                                                                     the 5'-end sequence/3'-end sequence is selected from those defised specification. The primer sets can be used in antisense therapy specification. The primers are useful for synthesising polynucle particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-CDNAs easily without any specialised methods. AAH0316 to AAH11631 represent human amino acid sequences; and AAH11631 to APH11632 to AAH11632 to AAH11632 to AAH11632 to AAH11632 to AAH11633 to AAH11632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 GVAERHGGIKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 GIADRAGGEKRGDQLLSVNGVSVEGEHHEKAVELLKAAQGKVKLVVRYTPKVLE
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2000US-00560875.
2000US-00598075.
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2000US-00654936.
2000US-00663561.
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2000US-00693325. 2000US-00728422

Xu C, Cao Y; , Chen R, Wang ZW; ndi V, Zhou P, Xh Zhang J, Ren F, Drmanac RT, Asumua Wang D, Wang J, Zhang J, QA, Wang D, Wang og Y, Wejhrman T, u C,

6283/51.

is encoding polypeptides with cytokine-like activities, useful and gene therapy

ge 370; 6221pp; English.

on relates to polynucleotides (AAK51456-AAK53435) and the peptides (AAM78323-AAM89302) that exhibit activity elating to all proliferantion or which may induce of other cytokines in other cell differentiation or which may induce of other cytokines in other cell populations. The des and polypeptides are useful in gene therapy, vaccines or apy. The polypeptides have various cytokine-like activities, all growth factor activity, haematopoiesis regulating sue growth factor activity, immunomodulatory activity and bin activity and may be useful in the diagnosis and/or carner, leukaemia, nervous system disorders, arthitis and on Note: Records for SEQ ID NO 2110 (AAK5581), 2111 and 3666 (AAM80020) are omitted as the relevant pages from the iting were missing at the time of publication

69.6%; Score 814; DB 4; Length 198; 80.6%; Pred. No. 1.6e-72; ive 24; Mismatches 13; Indels Conservative

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TLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNG 80

FRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPG 140 VRANATAKATVAAFAASEGHSHPRVVELPKTEEGLGFNIMGGKEQNSPIYISRIIPG 126 ERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARF 200

RTARREQ 211

|:|:|||| |RSAKRRQQ 197

ndard; protein; 207 AA.

(first entry)

ellular matrix and cell adhesion molecule-19 (XMAD-19).

disorder; acquired immune deficiency syndrome, AIDS; seease; allergy; anaemia; asthma; atheroselerosis; melanoma; asse; diabetes mellitus; atopic dermatitis; lymphoma; cancer; hiritis; multiple solerosis; Grave's disease; ostecarthritis; postriasis; rheumatoid arthritis; ulcerative colitis; '' genetic disorder; adrenoleukodystrophy; leukaemia; 'ome; cystic fibrosis; Gaucher's disease; myotonic dystrophy; anaemia; thalassaemia; autoimmune disorder; adenocarcinoma; cellular matrix and cell adhesion molecule; XMAD;

infection; cell proliferative disorder; actinic keratosis; myelc arteriosclerosis; nootropic; anticonvulsant; antithyroid; nephroneuroprotective; dermatological.

Homo sapiens

Location/Qualifiers Domain

91. .171 /note= "SH3 domain" 93. .174 Domain

/note= "PDZ domain"

WO200142285-A2

14-JUN-2001.

05-DEC-2000; 2000WO-US032990

99US-0172852P 10-DEC-1999; 16-DEC-1999;

(INCY-) INCYTE GENOMICS INC.

Burford N, Azimzai Y, Patterson C; P, Au-Young J; Lu DAM, Shah Lal P, Tang YT, Baughn MR, Yue H,

WPI; 2001-381632/40. N-PSDB; AAD08063 New human extracellular matrix and cell adhesion molecules and polynucleotide sequences encoding them, useful for diagnosis, prtreatment of genetic, autoimmune and cell proliferative disorder

Claim 1; Page 111-112; 135pp; English.

autoimmune/inflammatory disorders such as acquired immune defici syndrome (AIDS), Addison's disease, allergies, anaemia, asthma, atheroscierosis, Crohn's disease, diabetes mellitus, atopic derry glomerulonephritis, multiple sclerosis, Grave's disease, osteoan osteoporosis, psoriasis, rheumatoid arthritis, ulcerative coliti bacterial, fungal, parasitic, protozoal and helminthic infection cell proliferative disorders such as actinic keratosis, arterios and cancer including breast, bladder, bone marrow, brain and utcancer, leukaemia, adenocarcinoma, lymphoma, melanoma and myelom grander. The present sequence is a human extracellular matrix and cell ac molecule (XMAD). The XMAD is used for screening a compound for effectiveness as an agonist or antagonist of XMAD. The identifit or antagonist are used for treating a disease or condition assoc with decreased or increased expression of functional XMAD. The polynucleotides encoding XWAD are useful in somatic or germline therapy to express a conditions lethal genetic deficiency to express a conditions lethal gene product and to express a protein which affords prote against intracellular parasites and also for diagnosis of disor associated with expression of KWAD. They are also used for gene hybridisation probes useful in mapping the naturally occurring sequences and to create knock in humanised animals (pigs) or tre animals (mice or rats) to model human diseases. Oligonucleotide fragments derived from the polymucleotide sequences may be used elements on a microarray. Antibodies which specifically bind XM used for the diagnosis of disorders associated with the expressi diagnosed, prevented or treated include genetic disorders such adrenoleukodystrophy, Down's syndrome, cystic fibrosis, Gaucher' disease, myotonic dystrophy, sickle cell anaemia, thalassaemia, XMAD, or in assays to monitor patients being treated with XMAD.

Sequence 207 AA;

69.0%; Score 807; DB 4; Length 207; 78.5%; Pred. No. 8.4e-72; 17; Indels 24; Mismatches Best Local Similarity 78.58 Matches 157; Conservative Query Match

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The invention relates to one hundred and twenty two nucleic acid encoding PRO polypeptides. The sequences of the 122 PRO polynucl encode hunan secreted proteins. The PRO nucleic acids, polypeptic agonists and antagonists are useful for treating a PRO related (agonists and antagonists are useful for treating a PRO related (Inventument Colon cancer, breast tumour, prostate tumour, rectal tumour colon cancer, breast tumour, prostate tumour, rectal tumoring the proliferation of, or gene expression, in periorte cells, for stitle proliferation of differentiation of chondrocyte cells, for stitle proliferation of differentiation of chondrocyte cells, for stitle for stimulating or inhibiting the proliferation of normal human fibroblast cells. The PRO polypeptide may also be used as molect weight markers and for tissue typing. The PRO nucleic acids have applied may calculation and in chromosome and gene mapping, AAU83592-AAU83713 represent processing processing control of the invention
useful for treating a PRO related disorder and for diagnosing to as lung cancer, colon cancer, breast tumor, prostate tumor, rect or liver tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKE(
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                                                                                    Claim 11; Fig 76; 359pp; English.
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01-JUN-2001; 2001WO-US017800.
29-JUN-2001; 2001WO-US021066.
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        L--VEPLGLERDVSRAVELLERLQRSGELPPQKLQALQRVLQSRFCSAIREVYEQLY 58
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phan JF, Watanabe CK, Wood WI;
                                                                                                                            I I PGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL
                                              TVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ited protein; PRO; tumour; lung cancer; colon cancer; r; prostate tumour; rectal tumour; liver tumour; l proliferation; chondrocyte cell proliferation; sis factor-alpha.
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Smith V, Stephan JF,
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2000WO-US030873.
2000US-0253646P.
2000WO-US032678.
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2000WO-US034956.
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Gurney AL,
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Goddard A, Godowski PJ; shan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, esnoyers L, Gurney AL,

2045/32.

and twenty two nucleic acids encoding PRO polypeptides, he manufacture of a medicament for diagnosing or treating

76; 314pp; English.

RankohWahmenguuu Tido (*

invention relates to the isolation of novel human PRO and the polynucleotide sequences encoding them. The PRO are secreted and transmembrane proteins. The PRO and polynucleotides are useful for preparing a medicament ediagnosis and treatment of tumours. Anti-PRO antibodies are assort assays for PRO, by detecting its expression in 1s, tissues or serum, and for affinity purification of PRO nant cell culture or natural sources. ABUS0739-ABUS0800 e human PRO polypeptides of the invention. Note: The sequence spatent was obtained in electronic format directly from the te at seqdata.uspto.gov/psipsDIDEntry.html

AA;

2; Gaps 69.0%; Score 807; DB 6; Length 207; 78.5%; Pred. No. 8.4e-72; 17; Indels 24; Mismatches Conservative

LIVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 73 28 --VEPLGLERDVSRAVELLERLQRSGELPPQKLQALQRVLQSRFCSAIREVYEQIY 133 TVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY

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IIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193 VIPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVL 178

EARFEKLRTARREGOOG 213 EARFEKMRSARRQQHQ 198 ndard; protein; 207 AA.

(first entry)

secreted and transmembrane protein PRO10200.

c; osteopathic; gene therapy; TNF-Agonist-Alpha; stimulator; pericyte stimulator; fibroblast modulator; al; diagnostic; blosensor; bloreactor; tumour; lung tumour; preast tumour; prostate tumour; rectal tumour; bone disorder; cartilage disorder; sports injury; ted and transmembrane protein; PRO; cytostatic;

2002US-00218631.

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The invention describes an isolated nucleic acid molecule comprised sequence with at least 80% identity to: (a) a nucleotide encodin 122 PRO (secreted and transmembrane) polypeptides whose sequence fully defined in the specification; or (b) any of 122 nucleotide sequences having e.g. 4834, 2504 or 1759 bp fully defined in the specification; or the full length coding sequence of any these 1 nucleotide sequences. The PRO polypeptides or polynucleotides are specification; or the full length coding sequence of any these 1 nucleotide sequences. The PRO polypeptides or polynucleotides are as pharmaceuticals, diagnostics, biosensors or bioreactors. These particularly useful for detecting tumours (e.g. lung tumour, col tumour, breast tumour, prostate tumour, rectal tumour, or liver in a mammal, for stimulating the release of TMF-alpha from human for stimulating the proliferation or differentiation of chondroc cells, for stimulating proliferation or differation of chondroc cells, for stimulating proliferation or differation of control or for normal human dermal fibroblast proliferation. The PRO mucleic accompany particularly as to the presence of these diseases, and in the diagn determination of the presence of these diseases, and in the diagn alon useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes screening libraries of human cDNA, genomic DNA, genomic DNA, genomic DNA, genomic DNA or mRNA. The PRO gene. This is the amino acid sequence of a novel human secreted transmembrane PRO polypeptide
                                                                                                                             Godowski PJ,
                                                                                                                                                                                                                                                                           New genes, and its encoded secreted and transmembrane polypeptid useful for stimulating Tumor Necrosis Factor alpha, or chondrocy pericyte proliferation, especially for treating lung tumors, art
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                                                                                                                                               Gerritsen ME, Goddard A, Godowski F
Smith V, Stephan JF, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%; Score 807; DB 6; Length 207; 78.5%; Pred. No. 8.4e-72;
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                 01-JUN-2001; 2001MO-US017800.
29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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Matches 157; Conservative
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                                                                                                       (GETH ) GENENTECH INC.
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                                                                                                                                               Baker KP,
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macular degeneration; atherosclerosis; hypertension;
tenosis; rheumatoid arthritis, anglara; mycocardial infarction;
itis; lymphangitis; tumour angiogenesis; breast carcinoma;
oma; wound healing; chromosome mapping; gene mapping.
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                                                                                                                                                  ic; hypotensive; vulnenry; antiarteriosclerotic; ; cardiovascular disorder; endothelial disorder; isorder; cardiac hypertrophy; trauma; cancer;
secreted and transmembrane protein PRO10200.
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2000US-0220664P. 2001WO-US017800. 2001WO-US021066. 2002US-00219003.

NTECH INC.

2002US-00119480.

Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood WI; Gerritsen ME, Goddard Smith V, Stephan JF, esnoyers L, Gurney AL,

3229/37.

and eighty seven nucleic acids encoding PRO polypeptides, agnosis and treatment of cardiovascular (e.g. myocardial endothelial or angiogenic disorders in a mammal.

g 76; 314pp; English

on describes one hundred and eighty seven nucleic acids acids, thuman secreted and transmembrane (PRO) polypeptides. The acids, polypeptides, agonists and antagonists are useful for diagnosing a cardiovascular, endothelial or angiogenic a mammal, e.g. cardiac hypertrophy, trauma, cancer, agellar degeneration, atheroselersais, hypertension, atterial rheumatoid arthritis, angina, myocardial infartions, lits, lymphangitis, tumour angiogenesis (such as breast id liver carcinoma) and wound healing. The PRO nucleic acids tions in molecular blongy, including use as hybridisation in chromosome and gene mapping. This is the amino acid a novel human secreted and transmembrane PRO polypeptide

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                                                                                                                                                                     L--VEPLGLERDVSRAVELLERLQRSGELPPQKLQALQRVLQSRFCSAIREVYEQLY 58
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                                                                    Gaps
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69.0%; Score 807; DB 6; Length 207; 78.5%; Pred. No. 8.4e-72; ive 24; Mismatches 17; Indels
                                                                 Conservative
                                     larity
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134 ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRN

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The invention relates to a novel isolated nucleic acid encoding defined PRO polypeptide. The molecules of the invention may be to stimulating proliferation or gene expression in pericyte cells concludes of TMR-alpha from human blood. Other possible uses inclustimulation or inhibition of chondrocyte proliferation or inhibition of chondrocyte proliferation or califeration of the presence of a tumour with mammal. Furthermore, the nucleic acid may be useful for the mann of a medicament for diagnosing or treating a tumour within a man of a medicament for diagnosing or treating a tumour within a man of a control of the presence of a tumour within or a medicament for diagnosing or treating a tumour within a man of a during gene therapy. The current sequence is that of the human protein of the invention.
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Smith V, Stephan JF, Watanabe CK, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding for a PRO protein, useful for the man of a medicament for diagnosing or treating tumors or for measuridetecting expression of an associated gene.
                                                                                                                                                                                                                                                                         PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte differentiation; dermal fibroblast; tumour; gene therapy; cytost
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                                                                                                                             ABJ72265 standard; protein; 207 AA
                 179 EEMEARFEKWRSARRRQQHQ 198
194 EEMEARFEKLRTARRROOOO 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig 76; 315pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-2002; 2002US-00230414.
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09-APR-2002; 2002US-00119480.
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Grimaldi JC, Gurney AL,
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119 ISRVIPGGVADRHGGLKRGDQLLSVNGVSVBGEQHEKAVELLKAAQGSVKLVVRY Search completed: March 18, 2004, 13:26:52 Job time : 61 secs 179 EEMEARFEKMRSARRRQQHQ 198 194 EEMEARFEKLRTARRQQQQ 213 엄 à d IVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIY 133 /IPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVL 178 relates to a novel isolated PRO protein encoding nucleic sleic acid of the invention may be useful for preparing PRO and anti-PRO antibodies for detecting the presence of a nammal. Furthermore, the molecules of the invention may be timulating proliferation or gene expression in pericyte elease of tumour necrosis factor (TNF)-alpha from human roliferation or differentiation of chondrocyte cells and for he proliferation of normal human dermal fibroblast cells. molecules may be utilised during gene therapy. The current that of the human PRO protein of the invention IIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193 LIVVQPLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMH 73 Gerritsen ME, Goddard A, Godowski PJ; Smith V, Stephan JF, Watanabe CK, Wood WI; proliferation; pericyte cell; TNF alpha; chondrocyte; sis factor; proliferation; differentiation; gene therapy; 2; Gaps ๙ ain encoding nucleic acid, useful for preparing PRO and anti-PRO antibodies for detecting the presence of 69.0%; Score 807; DB 6; Length 207; 78.5%; Pred. No. 8.4e-72; Live 24; Mismatches 17; Indels ndard; protein; 207 AA. SARFEKLRTARROQOO 213 EARFEKMRSARRROOHO 198 3 76; 324pp; English. 2002US-00227884. 2001WO-US017800. 2001WO-US021066. 2002US-00119480 (first entry) Conservative senoyers L, Gurney AL, 00 protein. TECH INC. 3301/47. Larity olast.

 $\label{eq:continuous} \mathcal{L}_{\mathcal{C}}^{(i)} = \widehat{\mathbf{n}}, \qquad \qquad \mathbf{n} \quad \forall i \in \mathcal{T}, \mathcal{R} = \mathcal{L}.$

807 69.0 207 14 US-10-219-003-76 807 69.0 207 14 US-10-219-075-76 807 69.0 207 14 US-10-219-464-76 807 69.0 207 14 US-10-219-466-76 807 69.0 207 14 US-10-219-479-76 807 69.0 207 14 US-10-219-481-76 807 69.0 207 14 US-10-230-260-76 807 69.0 207 14 US-10-232-231-76 807 69.0 207 14 US-10-232-233-76 807 69.0 207 14 US-10-232-233-76	207 14 207 14 207 14 207 14 207 14 207 14 207 14	807 69.0 207 14 US-10-227-881-76 807 69.0 207 14 US-10-227-881-76 807 69.0 207 14 US-10-237-882-76 807 69.0 207 14 US-10-232-223-76 807 69.0 207 14 US-10-232-225-76 807 69.0 207 14 US-10-232-225-76 807 69.0 207 14 US-10-232-229-76 807 69.0 207 14 US-10-232-229-76 807 69.0 207 14 US-10-232-229-76	RESULT 1 US-09-909-005-1 US-09-909-005-1 Sequence 1, Application US/09909005 Patent No. USZOCO0020828BA1 SEQUENCE 1, APPLICANT: Yue, Henry APPLICANT: Are Henry APPLICANT: Are Henry APPLICANT: Patterson, Chandra TITLE OF INVENTION: CELL UNKCITON PDZ PROTEIN FILE REPRENCE: PF-05-99 US CURRENT FALING DATE: LOOL-07-18 PRIOR PPLICATION WUMBER: US/09/99,005 CURRENT FILING DATE: BALLIER FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PRI PROGRAMISM: Homo sapiens PEATURE: AT CORGANISM: Homo sapiens PEATURE: AD OTHER INFORMATION: 1974337 US-09-005-1 UMLENSTREAM OF THE PROGRAM
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. ein search, using sw model arch 18, 2004, 13:28:25; Search time 42 Seconds (without alignments) 1436.586 Million cell updates/sec	9909-005-1 PESVTSAPTADMATLTVVLLIG M62 10.0 , Gapext 0.5 177 seqs, 258955339 residues	<pre>ifs satisfying chosen parameters: 1049977 ingth: 0 ingth: 200000000 Minimum Match 0% Maximum Match 100% Listing first 45 summaries published applications at.*</pre>	:: / cgn2 6 /ptocate 1/2 /puppaa/USG6 NEW PUB. pep: *

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179 EEMBARFEKMRSARRRQOHQ 198
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       GKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                              ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ION: ACIDS ENCODING THE SAME
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ION NUMBER: 10/119,480
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ION NUMBER: 60/069873
ALE: 1997-12-17
ION NUMBER: 60/078910
ALE: 1997-12-17
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Imaldi, J. Christopher
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ATE: 1998-03-25
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUTITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: BYS30PLC103
FILE REFERENCE: BYS30PLC103
CURRENT APPLICATION NUMBER: US/10/232,230
CURRENT FILING DATE: 2002-08-29
FRIOR FILING DATE: 10/119,480
PRIOR APPLICATION NUMBER: 60/059113
FRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-12
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1998-03-26
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                                                                                                                                                                        Desnoyers, Luc
Gerriteen, Mary
Goddard, Audrey
Godowski, Paul J.
Grimald, J. Christopher
Gurney, Austin L.
Smith, Victoria
Stephan, Gan-Philippe F.
Waranabe, Colin L.
Wood, William I.
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Sequence 76, Application US/10232230 Publication No. US20040044180A1 GENERAL INFORMATION:
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Matches 157; Conservative
                                                                                                                                            APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo Sapien
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PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR APPLICATION NUMBER: 60/095316
PRIOR FILING DATE: 1996-08-10
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PRIOR FILING DATE: 1998-08-11
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PRIOR PLING DATE: 1998-12-22
PRIOR PLING DATE: 1998-12-23
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snoyers, Luc
rritsen, Mary
dard, Audrey
dowski, Paul J.
imaldi, J. Christopher
rney, Austin L.
ith, Victoria
ephan, Jean-Philippe F.
tanabe, Colin L.
od, William I.
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
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DATE: 2002-08-26
ION NUMBER: 10/119,480
ATE: 12002-04-09
ION NUMBER: 60/059113
ATE: 1997-09-17
ION NUMBER: 60/06287
ATE: 1997-10-28
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ATE: 1997-10-31
ION NUMBER: 60/064103
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ATE: 1998-04-15
ION NUMBER: 60/081855
ATE: 1998-04-15
ION NUMBER: 60/081855
ATE: 1998-04-15
ION NUMBER: 60/082804
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TION NUMBER: 60/091982
DATE: 1998-07-07
TION NUMBER: 60/095302
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MATE: 1998-05-22

TON NUMBER: 60/089532

MATE: 1998-06-17
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FION NUMBER: 60/090691
DATE: 1998-06
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:ION NUMBER: 60/090472
DATE: 1998-06-24
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NATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATE: 1998-04-22
IION NUMBER: 60/08441
ATE: 1998-05-06
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ATE: 1998-05-13
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US20030027988A1
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PEPLICANT DESCRIPTION TO CERTIFIED THE PEPLICANT DESCRIPTION CERTIFIED TO PEPLICANT CERTIFIED TO PEPRICANT CERTIFI
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Publication No. US20030036635Al
GENERAL INFORMATION:
                            194 EEMEARFEKLRTARRÇÇÇÇ 213
                                                           179 EEMEARFEXMRSARRQQHQ 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
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CON NUMBER: 60/115565

ATE: 1999-01-12

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ION NUMBER: 60/11573

ATE: 1999-02-10

ION NUMBER: 60/125619

ATE: 1999-03-19

ION NUMBER: 60/12575

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ION NUMBER: 60/16445

ATE: 1999-11-09

ION NUMBER: 60/166361

ATE: 1999-11-09

ION NUMBER: 60/166361
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DATE: 1998-12-15 TION NUMBER: 60/113296 DATE: 1998-12-22 TION NUMBER: 60/113605 ION NUMBER: 60/091982
ATE: 1998-07-07
ATE: 1998-07-07
ATE: 1998-08-04
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ION NUMBER: 60/095916
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ION NUMBER: 60/096791
ATE: 1998-08-17
ION NUMBER: 60/096791
ATE: 1998-08-17
ION NUMBER: 60/096791
ATE: 1998-08-17
ION NUMBER: 60/097986 ATE: 1998-09-10 :ION NUMBER: 60/099811 ATE: 1998-09-10 :ION NUMBER: 60/099812 ATE: 1998-09-10 DATE: 1998-09-11 FION NUMBER: 60/100385 DATE: 1998-00 DATE: 1998-09-10 TION NUMBER: 60/099816 DATE: 1998-09-10 FION NUMBER: 60/101741 DATE: 1998-09-24 FION NUMBER: 60/101786 DATE: 1998-11-18 FION NUMBER: 60/112422 TION NUMBER: 60/101738 DATE: 1998-10-28 FION NUMBER: 60/106248 DATE: 1998-10-30 FION NUMBER: 60/106905 DATE: 1998-11-03 TION NUMBER: 60/108787 TION NUMBER: 60/108849 TON NUMBER: 60/099596 NATE: 1998-09-09 TON NUMBER: 60/099598 NATE: 1998-09-09 CION NUMBER: 60/100038 NATE: 1998-09-11 TION NUMBER: 60/101477 ATE: 1998-09-23 : 1998-09-24 NUMBER: 60/101741 FION NUMBER: 60/101922 DATE: 1998-09-24 TION NUMBER: 60/106178 ATE: 1998-09-15 TION NUMBER: 60/100848 ION NUMBER: 60/100919 TION NUMBER: 60/101916 TION NUMBER: 60/106464 !ION NUMBER: 60/108801 : 1998-06-25 NUMBER: 60/091982 : 1998-07-07 ION NUMBER: 60/098544 ION NUMBER: 60/099803 ION NUMBER: 60/100627 9060/09 1998-10-29 1998-11-17 1998-09-16 1998-09-18 1998-09-25 ATE: 1998-09-24 1998-09-15 ATE: 1998-09-17 1998-08-3

| REIDER APPLICATION WINDSES: 66/11552
| PRIOR APPLICATION WINDSES: 66/11556
| PRIOR APPLICATION WINDSES: 66/11533
| PRIOR APPLICATION WINDSES: 66/11533
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| PRIOR PRIDRED DATE: 1999-04-25
| PRIOR PRIDRED DA

EARFEKURTARREQQQQ 213

plication US/10149819 US20030044913A1

YTE GENOMICS, INC.

E, Henry IMZAI, Yalda NG, Y. Tom

TTERSON, Chandra UGHN, Mariah R. , Dyung Aina M. AH, Purvi

-YOUNG, Janice RFORD, Neil

L, Preeti

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PRIOR APPLICATION NUMBER: 10/119,480

PRIOR FILING DATE: 2002-04-09

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059113

PRIOR APPLICATION NUMBER: 60/06287

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-10-28

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PRIOR APPLICATION NUMBER: 60/06813

PRIOR PILING DATE: 1997-12-17

PRIOR PILING DATE: 1998-03-20

PRIOR PILING DATE: 1998-03-25

PRIOR PELING DATE: 1998-03-25

PRIOR PELING DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27
APPLICANT: Goddard, Audrey

APPLICANT: Goddwski, Paul J.

APPLICANT: Goddwski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Smith, Victoria

APPLICANT: Smith, Victoria

APPLICANT: Matanabe, Colin L.

APPLICANT: Watanabe, Colin L.

APPLICANT: Worden Walliam I.

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REPERRANCE: PS330PLG92

CURRENT APPLICATION NUMBER: US/10/230,338

CURRENT FILING DATE: 2002-06-28
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US-10-218-631-76
Sequence 76, Application US/10218631
Publication No. US20330045687A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Gerriteen, Mary
APPLICANT: Goddard, Addrey.
APPLICANT: Goddwski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
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LENGTH: 207
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                                                                                                                           VIPGGVADRHGGLKRGDQLLSVNGVSVEGEQHEKAVELLKAAQGSVKLVVRYTPRVI 178
           DITGSAEIRAHATAKATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKEQNSPIY 118
                                                                                 II PGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
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larity 78.5%; Pred. No. 5.5e-70;
Conservative 24; Mismatches 17; Indels 2
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TION: Incyte ID No. US20030044913A1 4062841CD1
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DATE: 2002-06-10 ION NUMBER: 60/172,852; 60/172,354 ATE: 1999-12-10; 1999-12-16 ID NOS: 42

o sapiens

EARFEKLRTARRROOOD 213

oplication US/10230338 US20030044934A1 VTION:

cer, Kevin P. snoyers, Luc rritsen, Mary

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APPLICANT: Macainal, Colling 1.

APPLICANT: Macainal, Colling 1.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NITTLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SPECEMENT PELINGS DATE: 2002-08-28

CURRENT FILING DATE: 2002-08-28

PRIOR PELING DATE: 2002-04-09

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-17

PRIOR PELING DATE: 1997-10-28

PRIOR PELING DATE: 1997-10-28

PRIOR PELING DATE: 1997-10-28

PRIOR PELING DATE: 1997-10-31

PRIOR PELING DATE: 1997-12-17

PRIOR PELING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/06913

PRIOR PELING DATE: 1998-03-20

PRIOR PELING DATE: 1998-03-20

PRIOR PELING DATE: 1998-03-26

PRIOR PELING DATE: 1998-03-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 78.5%; Pred. No. 5.5e-70;
Matches 157; Conservative 24; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goddard, Audrey,
APPLICANT: Goddward, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watenabe, Coan-Philippe F.
APPLICANT: Watenabe, Coan-Philippe F.
APPLICANT: Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 EEMEARFEKURSARRRQQHQ 198
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APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                 TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TION: ACIDS ENCODING THE SAME
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ID NOS: 246
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ATION NUMBER: US/10/218,631
                                                                                                                                                                                                                                                                                                                                                                                                                 TON NUMBER: 10/119,480
ATE: 202-04-09
TON NUMBER: 60/059113
ATE: 1997-09-17
TON NUMBER: 60/062287
ATE: 1997-10-17
TON NUMBER: 60/06354
ATE: 1997-10-28
ATE: 1997-10-38
ATE: 1997-10-31
TON NUMBER: 60/069873
ATE: 1997-12-17
TON NUMBER: 60/069873
ATE: 1997-12-17
TON NUMBER: 60/079294
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rney, Austin L.
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ephan, Jean-Philippe F.
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ION NUMBER: 60/079656

ATE: 1998-03-26

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ATE: 1998-03-27
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od, William I.
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oddard, Audrey
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ELICANT GOODSKY, NALY

PELICANT GOODSKY, NALY

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CURRENT APPLICATION NUMBER. US/10/227, 873

CURRENT FILING DATE . 2002-04-06

FRIOR PELICATION NUMBER. 10/119, 480

PRIOR PELICATION NUMBER. 60/052113

PRIOR PELICATION NUMBER. 60/052149

PRIOR PELICATION NUMBER. 60/072294

PRIOR PELICATION NUMBER. 60/072294
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                                                                                                                                                                                                                                                                                                                                       Length 207;
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                          Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 76
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                   Query Match 69.0%; Score 807; DB 14; Best Local Similarity 78.5%; Pred. No. 5.5e-70; Matches 157; Conservative 24; Mismatches 17;
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Publication No. US20030073816A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 EEMEARFEKLRTARRQQQQ 213
       CURRENT FILING DATE: 2002-08-12
                                                                                                                                                                                                                            ; ORGANISM: Homo Sapien
US-10-218-849-76
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ith, Vatoria
phan, Jean-Philippe F.
canabe, Colin L.
od, William I.
IION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FION: ACIDS ENCODING THE SAME
                                                                                                   DATE: 2002-08-09

CIN NUMBER: 10/119,480

CIN NUMBER: 0/052-08-09

CIN NUMBER: 60/059113

CIN NUMBER: 60/06287

CON NUMBER: 60/06287

CON NUMBER: 60/063549

CIN NUMBER: 60/064103

CIN NUMBER: 60/06973

CIN NUMBER: 60/06973

CIN NUMBER: 60/078910

CON NUMBER: 60/078910

CON NUMBER: 60/078910

CON NUMBER: 60/079294

CIN NUMBER: 60/079294

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TON: ACIDS ENCODING THE SAME P3530P1C6 TION NUMBER: US/10/216,159A
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ATION NUMBER: US/10/218,849
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critsen, Mary
Jdard, Audrey
Jdaski, Paul J.
imaldi, J. Christopher
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er, Kevin P.

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TOWN NUMBER 60/081955

TOWN NUMBER 60/08284

ON NUMBER 60/08284

ON NUMBER 60/08232

ON NUMBER 60/08232

ON NUMBER 60/08292

ON NUMBER 60/09298

ON NUMBER 60/09298

ON NUMBER 60/09298

ON NUMBER 60/09292

ON NUMBER 60/09298

ON NUMBER 60/09398

O

PRIOR FILING DATE: 1996-09-24

PRIOR FILING DATE: 1996-02-4

PRIOR FILING DATE: 1996-02-4

PRIOR FILING DATE: 1996-02-24

PRIOR FILING DATE: 1996-02-24

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PRIOR PLING DATE: 1996-10-29

PRIOR APPLICATION NUMBER: 60/106748

PRIOR PLING DATE: 1996-10-29

PRIOR APPLICATION NUMBER: 60/10690

PRIOR PLING DATE: 1998-10-30

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PRIOR PLING DATE: 1999-01-13

PRIOR PLING DATE: 1999-01-13

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Conservative

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PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/09195
PRIOR APPLICATION NUMBER: 60/081919
PRIOR FILING DATE: 1998-04-15
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PRIOR APPLICATION NUMBER: 60/08532
PRIOR PILING DATE: 1998-05-13
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PRIOR PILING DATE: 1998-05-16
PRIOR PILING DATE: 1998-05-17
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-16
PRIOR PILING DA
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od, William I.

TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
:: P3530PL78:
ATION NUMBER: US/10/227,883
                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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rritsen, Mary
dowski, Paul J.
inaldi, J. Christopher
rney, Austin L.
ith, Victoria
ephan, Jean-Philippe F.
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ION NUMBER: 60/078910
NATE: 1998-03-20
ION NUMBER: 60/079294
AATE: 1998-03-25
ION NUMBER: 60/079656
  ION NUMBER: 60/149638
ATE: 1399-08-17
ION NUMBER: 60/151733
ATE: 1999-08-31
ION NUMBER: 60/164418
ATE: 1999-11-09
ION NUMBER: 60/166361
ATE: 1999-11-16
ION NUMBER: 60/169445
ATE: 1999-12-07
ION NUMBER: 60/169495
ATE: 1999-12-07
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ION NUMBER: 60/169495
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ION NUMBER: 10/119,480
ATE: 2002-04-09
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'ION NUMBER: 60/064103

ATE: 1997-10-31

'ION NUMBER: 60/069873
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ION NUMBER: 60/063549
ATE: 1997-10-28
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ION NUMBER: 60/062287
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er, Kevin P.

TION NUMBER: 60/108787 JATE: 1998-11-17 TION NUMBER: 60/10861 JATE: 1998-11-17 TION NUMBER: 60/108849 JATE: 1998-11-18 TION NUMBER: 60/113296 JATE: 1998-12-22 TION NUMBER: 60/113296 JATE: 1998-12-22 TION NUMBER: 60/113605 JATE: 1998-12-23 TION NUMBER: 60/11361 JATE: 1998-12-23 TON NUMBER: 60/101738

ATE: 1998-09-24

TON NUMBER: 60/101741

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TON NUMBER: 60/101766

ATE: 1998-09-25

TON NUMBER: 60/101916

ATE: 1998-09-24

TON NUMBER: 60/10192

ATE: 1998-09-24

TON NUMBER: 60/10192

ATE: 1998-19-24

TON NUMBER: 60/10192

ATE: 1998-10-28 TON NUMBER: 60/115558
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TION NUMBER: 60/115733
DATE: 1999-01-12
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DATE: 1999-03-19
FION WUMBER: 60/125775
DATE: 1999-03-23
IION NUMBER: 60/126773 IION NUMBER: 60/145698 DATE: 1999-07-26 IION NUMBER: 60/146222 FION NUMBER: 60/106248 NATE: 1998-10-29 TION NUMBER: 60/123618 DATE: 1999-03-10 DATE: 1999-04-05 FION NUMBER: 60/130232 DATE: 1999-04-21 DATE: 1999-04-27 FION NUMBER: 60/131445 DATE: 1999-04-28 DATE: 1999-05-14 TION NUMBER: 60/140650 FION NUMBER: 60/144758 CATE: 1999-07-20 ION NUMBER: 60/106905 NATE: 1998-11-03 MATE: 1999-03-29 DATE: 1999-04-26 CION NUMBER: 60/131270 DATE: 1999-04-27 FION NUMBER: 60/131291 LION NUMBER: 60/140723 DATE: 1999-06-22 ION NUMBER: 60/106464 ATE: 1998-10-30 FION NUMBER: 60/134287 TION NUMBER: 60/141037 ION NUMBER: 60/131022 1999-02-10 DATE: 1999-06-23 DATE: 1999-06-22

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APPLICANT: Barciteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Gerriteen, Mary
APPLICANT: Gedward, Audrey
APPLICANT: Godward, Audrey
APPLICANT: Godward, Audrey
APPLICANT: Godward, Austin 1.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wadd, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND N
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION NUMBER: 10/119, 480
FRIOR FILING DATE: 1097-10-17
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-10-31
FRIOR FILING DATE: 1997-110-31
FRIOR FILING DATE: 1997-110-31
FRIOR FILING DATE: 1997-110-31
FRIOR FILING DATE: 1997-110-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 ETITVNGCPEFRARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 DILDITGSAEIRAHATAKATVAAFTASEGHAHPRVVELPKTDEGLGFNIMGGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 ISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.0%; Score 807; DB 14; Length 207; Best Local Similarity 78.5%; Pred. No. 5.5e-70; Matches 157; Conservative 24; Mismatches 17; Indels
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
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PRIOR PLICATION NUMBER: 60/149320
PRIOR PRILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR PLICATION DATE: 1999-08-13
PRIOR PLICATION NUMBER: 60/16133
PRIOR FILING DATE: 1999-11-09
PRIOR PLICATION NUMBER: 60/16418
PRIOR PLICATION NUMBER: 60/16418
PRIOR PLICATION NUMBER: 60/16418
PRIOR APPLICATION NUMBER: 60/166361
PRIOR PLICATION NUMBER: 60/169455
PRIOR PLILING DATE: 1999-11-16
PRIOR PLILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 76, Application US/10219076; Publication No. US20030078379A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baker, Kevin P.
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US-10-219-076-76
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PRIOR PLING DATE: 1998-09-15
PRIOR PLING DATE: 1998-09-15
PRIOR PLING DATE: 1998-09-15
PRIOR PLING DATE: 1998-09-16
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dard, Audrey
ddard, Audrey
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ddard, Paul J.
imaldi, J. Christopher
irney, Austin L.
ith, Victoria
ephan, Jean-Philippe F.
tanabe, Colin L.
od, William I.
TION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TION: ACIDS ENCODING THE SAME
: P3530B1C82
STION NUMBER: US/10/230,434
: DATE: 2002-08-28
ION NUMBER: 10/119,480
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ION NUMBER: 60/078910
)AFE: 1998-03-20
ION NUMBER: 60/079294
)ATE: 1998-03-25
ION NUMBER: 60/07956
)ATE: 1998-03-36
ION NUMBER: 60/079728
)ATE: 1998-03-27
ION NUMBER: 06/079728
IDN NOBER: 60/079728
IDN NOS: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                             69.0%; Score 807; DB 14; Length 207;
larity 78.5%; Pred. No. 5.5e-70;
Conservative 24; Mismatches 17; Indels 7;
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ATE: 1997-12-17
10N NUMBER: 60/078910
ATE: 1998-03-20
10N NUMBER: 60/079294
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ION NUMBER: 60/062287
ATE: 1997-10-17
ION NUMBER: 60/063549
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ION NUMBER: 60/064103
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TION NUMBER: 60/101477
DATE: 1998-09-23
TION NUMBER: 60/101741
DATE: 1998-09-24
TION NUMBER: 60/101741
DATE: 1998-09-25
TION NUMBER: 60/101916
DATE: 1998-09-25
TION NUMBER: 60/101912
DATE: 1998-10-29
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DATE: 1998-10-29
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DATE: 1998-10-29
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DATE: 1998-11-17
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TION NUMBER: 60/10801
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TION NUMBER: 60/113621
DATE: 1999-10-12
TION NUMBER: 60/113621
DATE: 1999-01-12
TION NUMBER: 60/113621
TION NUMBER: 60/11363
TION NUMBER: 60/11363
TION NUMBER: 60/11363
TION NUMBER: 60/11465
DATE: 1999-06-22
TION NUMBER: 60/114758
TION NUMBER: 60/14758

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14 MATLTVVQPITLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 completed: March 18, 2004, 13:34:03
PRIOR FILING DATE: 1999-07-26
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PRIOR APPLICATION NUMBER: 60/146963
PRIOR APPLICATION NUMBER: 60/146963
PRIOR APPLICATION NUMBER: 60/149320
PRIOR PILING DATE: 1999-08-03
PRIOR FILING DATE: 1999-08-17
PRIOR PRILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/14938
PRIOR APLICATION NUMBER: 60/14938
PRIOR APLICATION NUMBER: 60/16418
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PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-11-16
PRIOR PILING DATE: 1999-12-07
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Sequence Sequence Sequence

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237 RHGGLKRGDQLIAVNG-NVEAECHEKAVDLLKSAVGSVKLVIRYMPKLLDEMERI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 RARATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 RHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 PRVVELPKTDEGLGFNVMGGKEQNSPIXISRIIPGGVAERHGGLKRGDQLLSVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.0%; Score 643.5; DB 3; Length 297; 70.6%; Pred. No. 2e-56; Live 29; Mismatches 23; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 196.5; DB 4; Length 7;
; Pred. No. 4.5e-11;
19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gottherdt, Michael
TILLE ON TINVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
                                                                                    RESULT 4
US-09-30-102-3
Sequence 3, Application US/09370102
Patent No. 6265547
GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Chandra
: TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
: FILE REFERENCE: PF-0599 US
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/370,102
CURRENT FILING DATE: 1999-08-06
EARLIER APPLICATION NUMBER: 09/151,611
EARLIER FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-562-737-21
Sequence 21, Application US/09562737
; Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%;
41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE: -
; OTHER INFORMATION: 91685067
US-09-370-102-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.0%
Best Local Similarity 70.6%
Matches 127; Conservative
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Best Local Similarity 41.4%
Matches 41; Conservative
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LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGKEQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATAKATVAAFAAAAGHAHPRIVELPKTDQGLGFNVMGGKEQNSPIYISRIIPGGVAD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAKATVAAFAASEGHSHPRVVELPKTDEGLGFNVMGGKEQNSPIYISRIIPGGVAE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQXMHETITVNGCPEF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                             PSVTSAPTADMATLTVVQPLTLDRDVARAIELLEKQQESGEVPVHKLQSLKKVLQSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1170; DB 3; Length 233; larity 100.0%; Pred. No. 2.5e-109; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%; Score 643.5; DB 2; Length 297; larity 70.6%; Pred. No. 2e-56; Conservative 29; Mismatches 23; Indels 1
             TION: CELL JUNCTION PDZ PROTEIN
TION: CELL JUNCTION PDZ PROTEIN
STION NUMBER: US/09/370,102
DATE: 1999-08-06
ATION NUMBER: 09/151,611
ID NOS: 3
Program
Program
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Young, Janice
terson, Chandra
TION: CELL JUNCTION PDZ PROTEIN
: PR-0599 US
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ID NOS: 3
Program
Chandra
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                                                                                                                                                                                                                                                                                                 TION: 1974337
                                                                                                                                                                                                                                                      no sapiens
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GENERAL INFORMATION:
APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN/ CARL-HERNRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOW
TITLE OF TRYENTON: TYROSINE PHOSPHATASES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 -- EQNSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1094 KMETDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLEGVSHHAAIEILQNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 PLTLDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 15.7%; Score 184; DB 2; Length 2465; l Similarity 28.6%; Pred. No. 4.6e-09; 52; Conservative 30; Mismatches 64; Indels 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 PEFRARATAKATV----AAFAASEGHSHPRVVELPKTD----
             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERCHILIN RELEASE #1.0, Version #1.25
SUBSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        993 PQTVAELVGKPSHQMSRSDAESLAGVTKLNNSKSV----
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                                                                                            FILING DATE: 09-A00-1996
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION DATE: 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: 10461/7000
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/09100804; Patent No. 6066472
                                                                                                                                                                                                                                                                                                                                            IFLEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 Amir-
                                                                                                                                                                                                                                                                                                                                                                                                                                        : 2465 amino acids amino acid
                                                                                                                                                                                                                                                                                                         LECCRETCHONE: 61///___TELEPHONE: 61//720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-596-291-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASSACHUSETTS: USA
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Best Local Similarity
Matches 52; Conserv
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1154 VI 1155
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STREET: 600
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TETPPPKIITLEKGSEGLGFSIVGGYGSPHGDLPIYVKTVFAKGAAADDGRLKRGDQI 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOPLDGLSHADVVNLLKNAYGRIILQVVADTNISALAAQLENMSTGYHLGSPTAEHHP 1789
RIVIHRGSTGLGFNIVGG-EDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3CP-----SEGHS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PRVVELPKTDEGLGFNVMGG---KEQNSPIYISRIIPGGVAERHGGLKRGDQL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIMARY STRUCTURE AND FUNCTIONAL EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETIT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.2%; Score 190; DB 4; Length 1881; 25.6%; Pred. No. 7.9e-10; .ive 36; Mismatches 61; Indels 6
                                                                                                                                                                                                                                                                 rtel, Paul L.
vtigian, Sean V.
riad Genetics, Inc.
WILON: MMSC1 - An MWAC1 Interacting Protein
                                                                          HEKAVELLKAAKDSVKLVVRYTPKVLEEMEARFEKLR 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                          B: MMSCI Gene
CATION NUMBER: US/09/233,086
                                                                                                                                                                                                                                                                                                                                                                                                        G DATE: 1999-01-19
CATION NUMBER: US 60/071,861
G DATE: 1998-01-20
ID NOS: 65
                                                                                                                                                                                                     plication US/09233086
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HELDIN, CARL-HENRIK
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PE: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entin Ver. 2.0
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IELLEKLOES----

mo sapiens

ASSACHUSETTS USA

TCE ADDRESS

SOUENCES:

ZENTION: ENTION:

SARAS, JAN

36;

TION:

1155 186

linear E: prot

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SRLDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLEGVSHHAAIEILQNAPEDVT 1153
                                                                                                                                                                                                                                                     VAELVGKPSHQMSRSDAESLAGVTKLNNSKSV-------ASLNRS 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                              PARATAKATV----AAFAASEGHSHPRVVELPKTD------EGLGFNVMGGK 126
                                                                                                                                                                                                                                                                                                                                                                             ---NSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEHHEKAVELLKAAKDSVK 183
                                                                                                                                                                                                                  LDRDVARAIELLEKLQESGEVPVHKLQSLKKVLQSEFCTAIREVYQYMHETITVNGC 81
                                                                                                                                  15.4%; Score 180.5; DB 4; Length 2466; 27.9%; Pred. No. 1e-08; tive 31; Mismatches 64; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIMARY STRUCTURE AND FUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
LICATION DATA:
ON NUMBER: PCT/US94/09943
TE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMEY, MICHAEL J.
ION NUMBER: P-38,349
/DOCKET NUMBER: LO461/7000WO
CATION INFORMATION:
SEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
ADABLE FORM:
PE: Floppy disk
IBM PC comparible
"""EM: PC-DOS/MS-DOS
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ON NUMBER: US 08/115,573
IE: 01-SEP-1993
ENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plication PC/TUS9409943 WATION:
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500 ATLANTIC AVENUE
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617/720-2441
2-1742 EZEKIEL
OR SEQ ID NO: 2:
(ARACTERISTICS:
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ino acid
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                                                                                no sapiens
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117 GLGFNVMGGKEQ---NSPIYISRIIPGGVAERHGGLKRGDQLLSVNGVSVEGEH
                                                                                                                                                                                                                                                         5 GLGFQIIGGEKMGRLDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLEGVS
             Query Match
14.7%; Score 172.5; DB 3; Length 77;
Best Local Similarity 47.9%; Pred. No. 4.6e-10;
Matches 35; Conservative 16; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 18, 2004, 13:29:27 Job time: 23 secs
                                                                                                                                                                                                                                                                                                                                                                            174 LLKAAKDSVKLVV 186
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HELDIN, CARL-HENRIK
ENTION: PRIMARY STRUCTURE AND FUNCTIONAL
ENTION: EXPRESSION OF NUCLECTIDE SEQUENCES FOR NOVEL PROTEIN
ENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
ATION: Description of Artificial Sequence: Synthetic ATION: Sequence
                                                                                                                                                                      14.8%; Score 173.5; DB 4; Length 724; larity 39.4%; Pred. No. 9.1e-09; Conservative 18; Mismatches 38; Indels I.
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TE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PATENTIN Release #1.0, Version #1.25
ICATION DATA:
N NUMBER: US/09/100,804
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N NUMBER: US 08/596,291

E. 09-AUG-1996

TI ON DEP-1993

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N NUMBER: PCT/US94/09943

E: 01-SEP-1994

E: 01-SEP-1994

N NUMBER: PCT/US94/09943

E: 01-SEP-1994

N NUMBER: LO4661/7003

ATTON INFORMATION:

ES, EDWARD R.

ON NUMBER: 31,616

DOCKET NUMBER: LO461/7003

ATTON INFORMATION:
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RACTERISTICS:
7 amino acids
no acid
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